

**FIG. 2**

BHR (PC20  $\leq$  16 mg/ml) & Asthma

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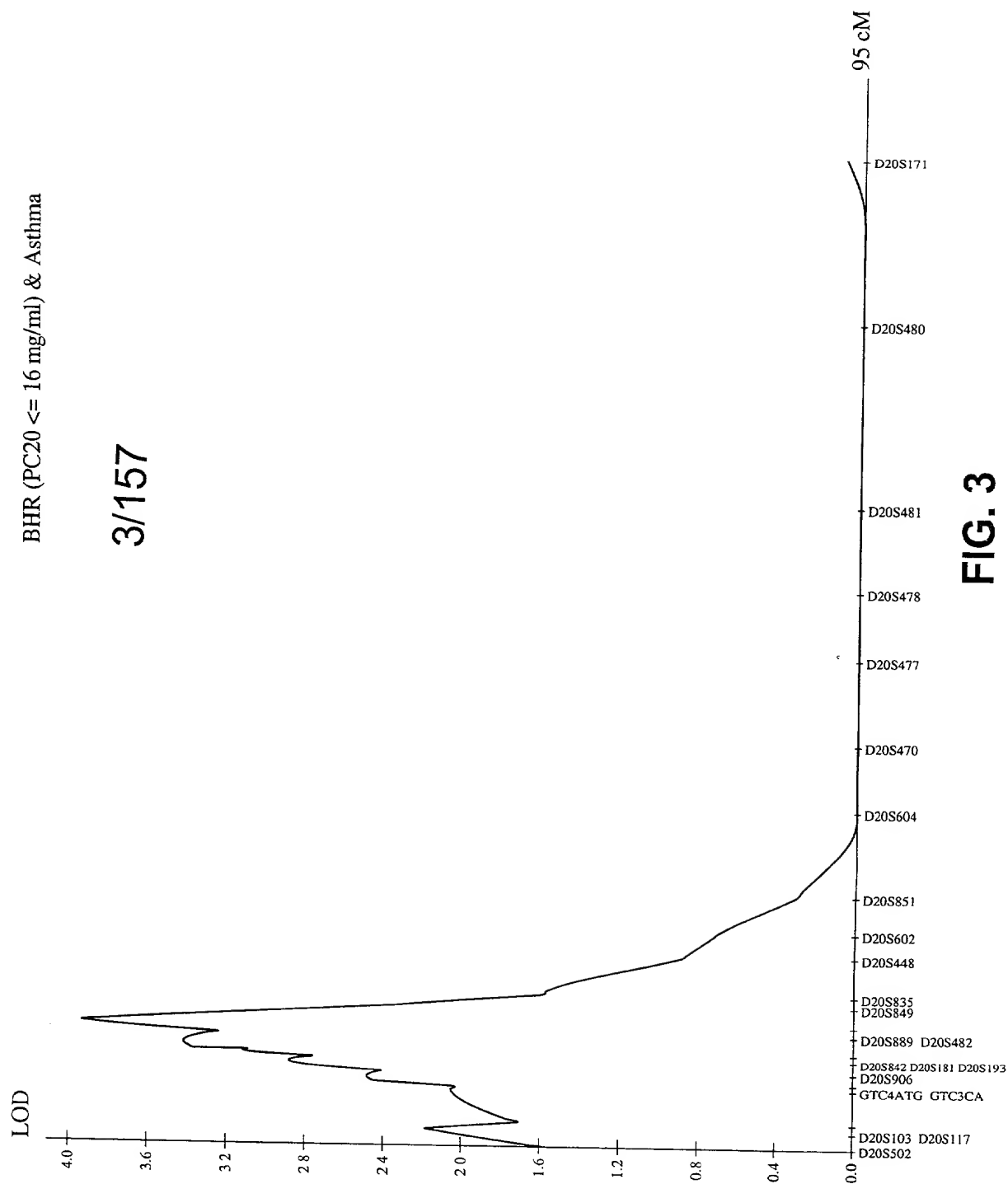
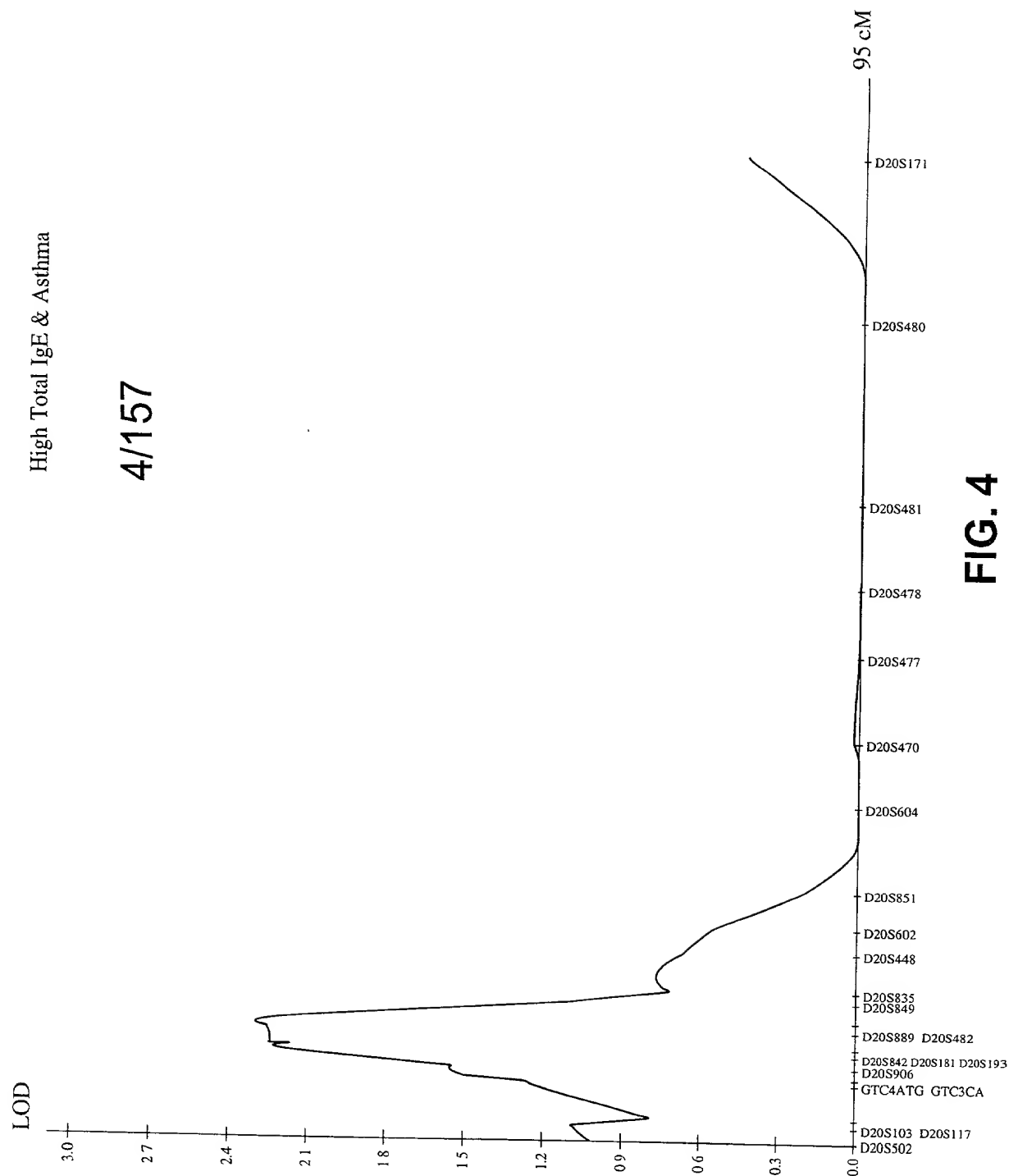


FIG. 3

High Total IgE & Asthma

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# High Specific IgE & Asthma

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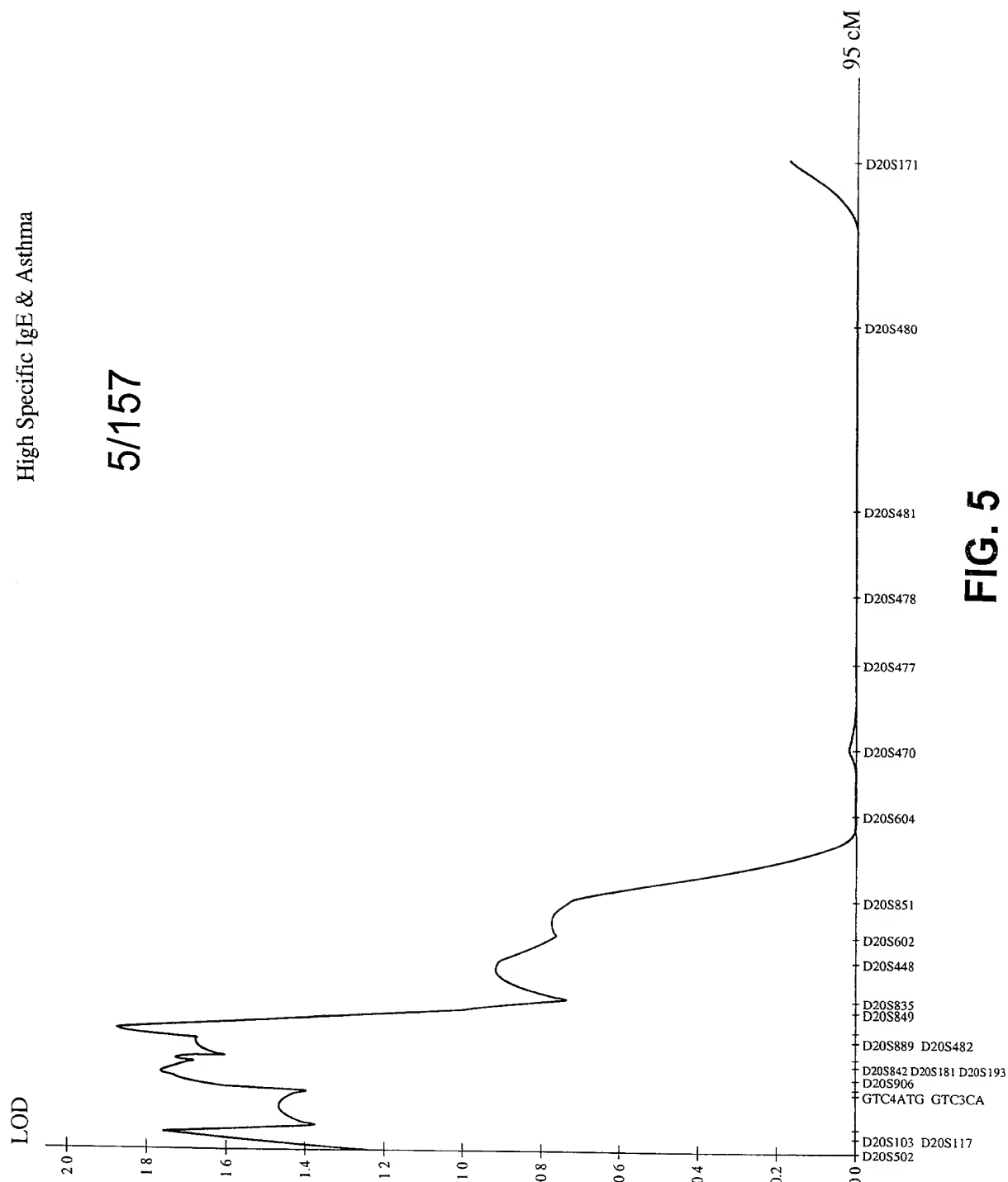


FIG. 5

**FIG. 6**

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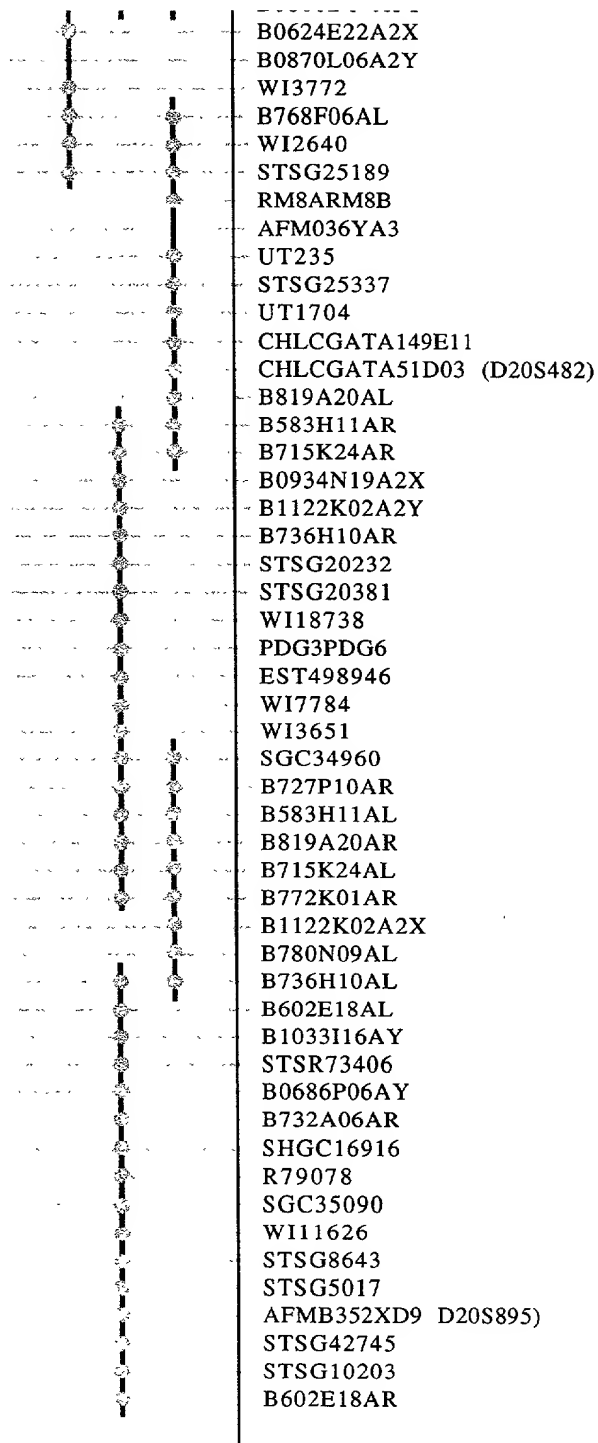


FIG. 6

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>BAC1098L22 sequence

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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7



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FIG. 7

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FIG. 7

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FIG. 7

**FIG. 7**

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FIG. 7

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FIG. 7

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FIG. 7



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FIG. 7



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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7



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FIG. 7



FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7



**FIG. 7**



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FIG. 7

**FIG. 7**

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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

**FIG. 7**



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FIG. 7



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FIG. 7



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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7



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FIG. 7



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FIG. 7

**FIG. 7**

cccaggaggtggaggggtgcagtttaactgaaattgtgcccactacactccagccagggtgacaaaacaagactcttctctca  
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FIG. 7

**FIG. 7**

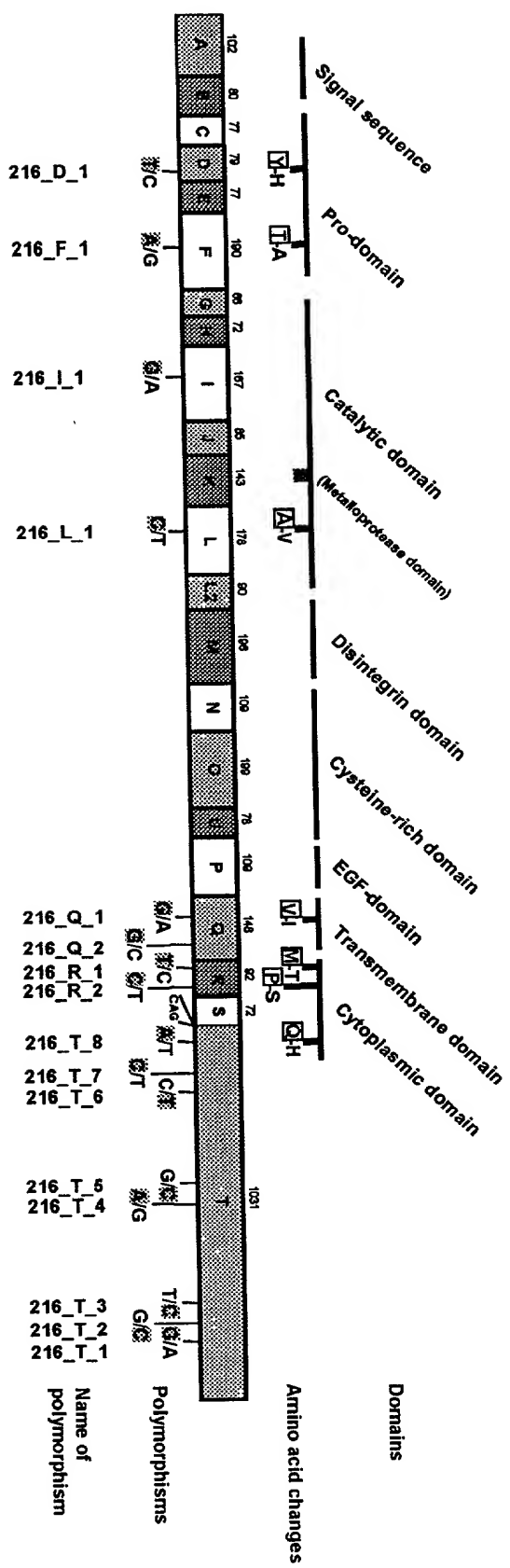


FIG. 8

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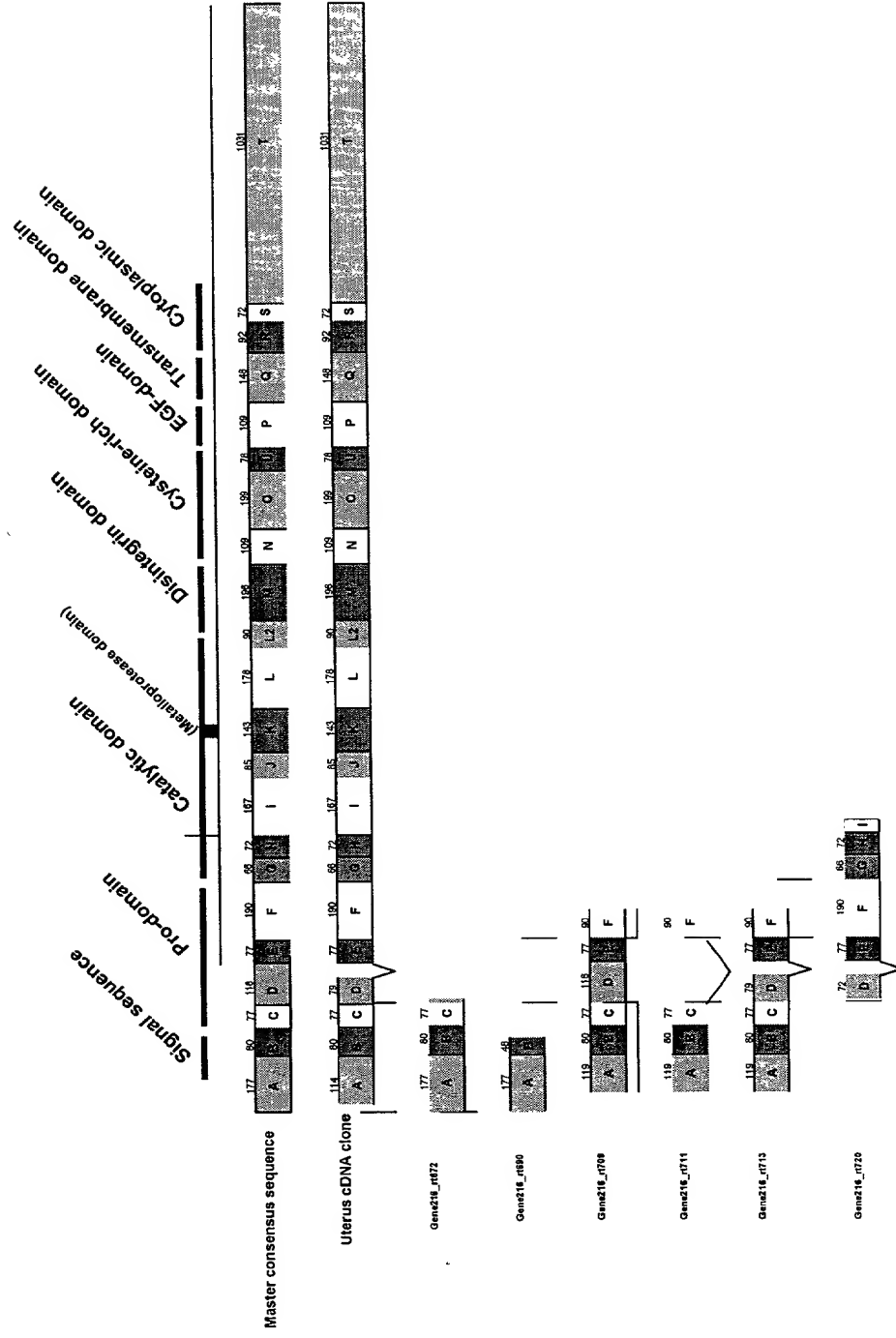


FIG. 9

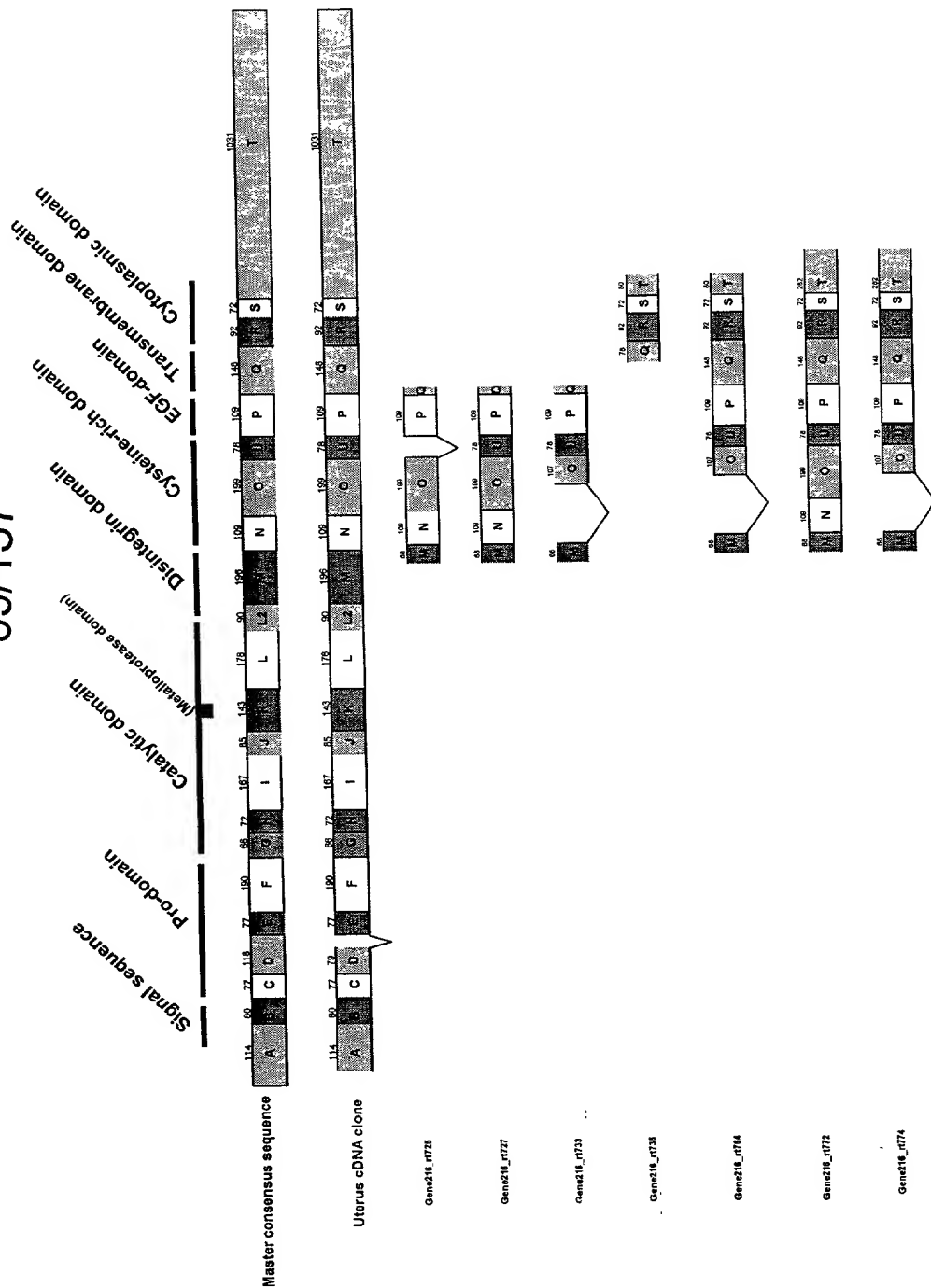
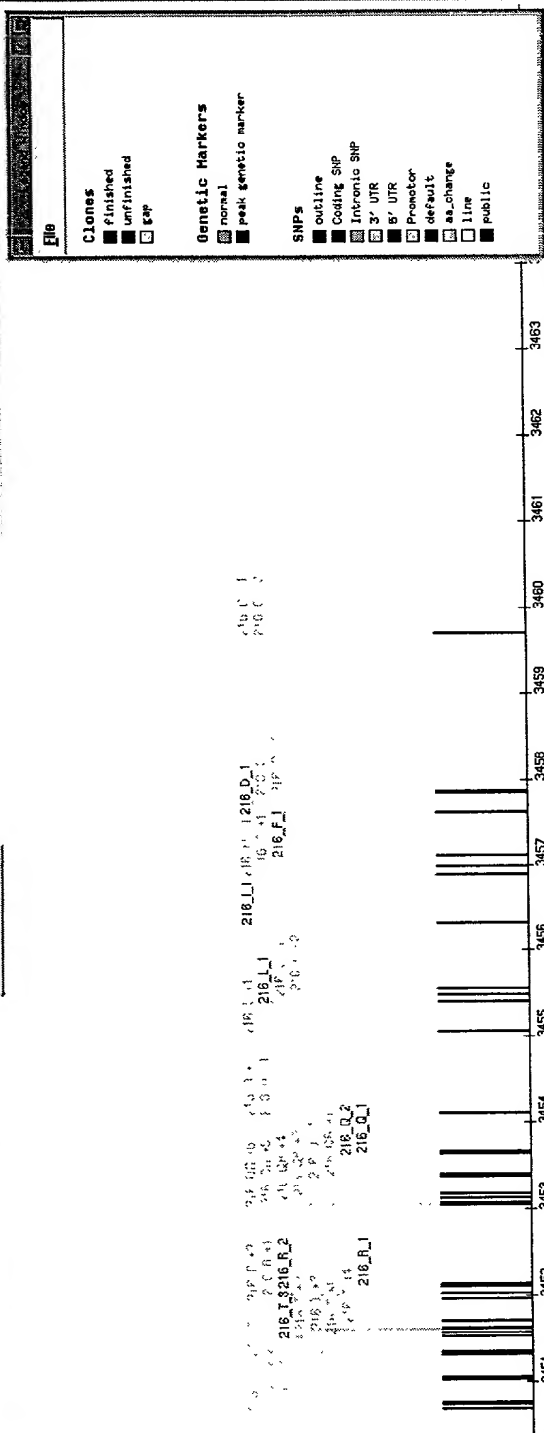


FIG. 10

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216\_promoter  
216\_mouse

216\_T  
216\_S  
216\_R  
216\_Q  
216\_P  
216\_O  
216\_N  
216\_M  
216\_L  
216\_K  
216\_J  
216\_I  
216\_H  
216\_G  
216\_F  
216\_E  
216\_D  
216\_C  
216\_B  
216\_A

FIG. 11



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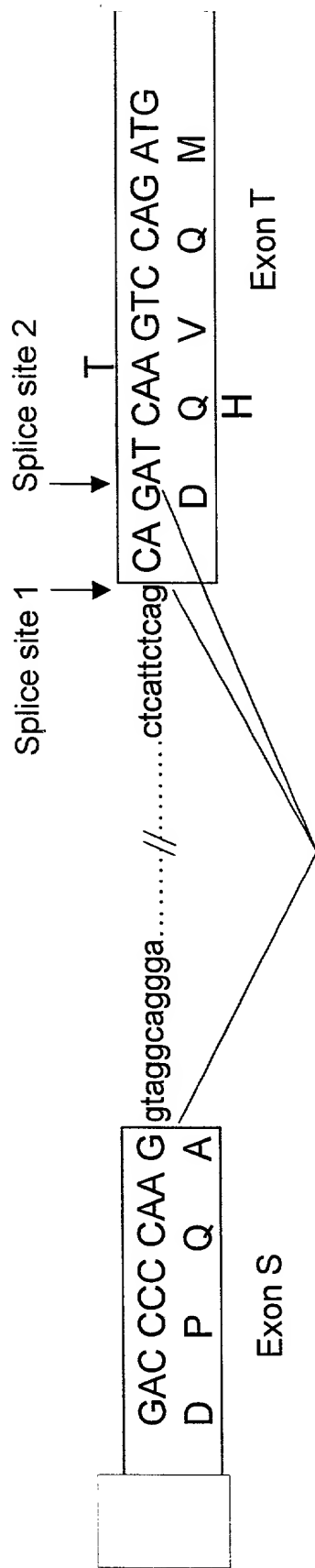


FIG. 12

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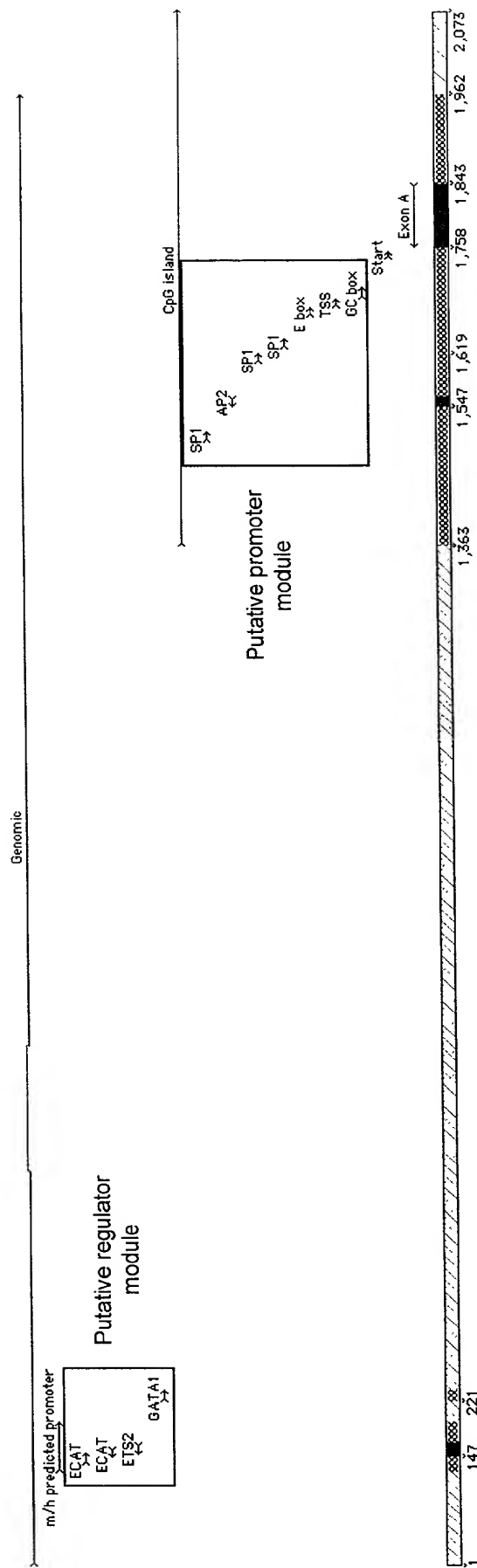


FIG. 13

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Branch of the ADAM family that Gene 216  
is closely related to

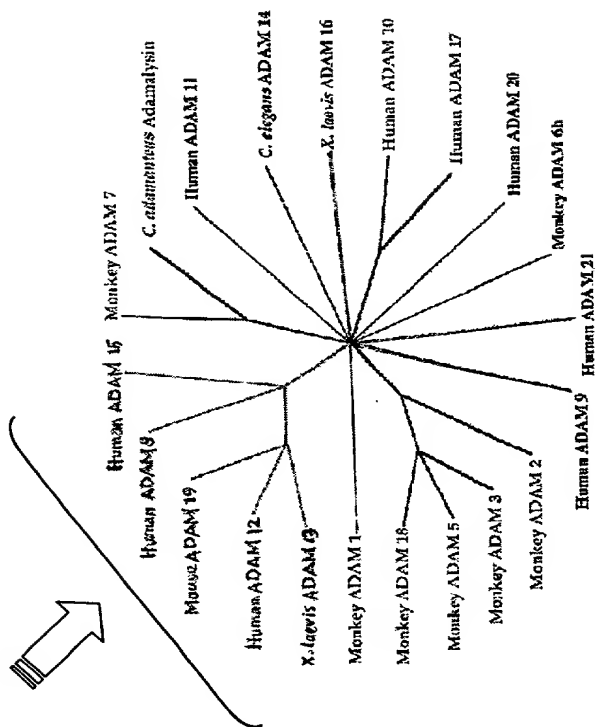
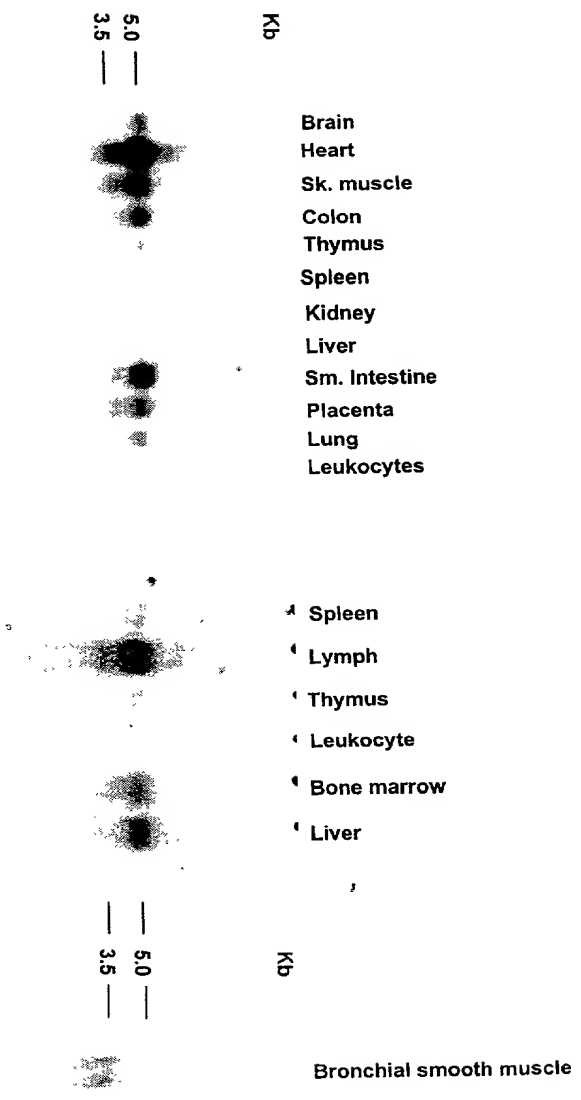


FIG. 14

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**FIG. 15**

	1990-1991	1991-1992	1992-1993	1993-1994	1994-1995	1995-1996	1996-1997	1997-1998	1998-1999	1999-2000	2000-2001	2001-2002	2002-2003	2003-2004	2004-2005	2005-2006	2006-2007	2007-2008	2008-2009	2009-2010	2010-2011	2011-2012	2012-2013	2013-2014	2014-2015	2015-2016	2016-2017	2017-2018	2018-2019	2019-2020	2020-2021	2021-2022	2022-2023	2023-2024	2024-2025	2025-2026	2026-2027	2027-2028	2028-2029	2029-2030	2030-2031	2031-2032	2032-2033	2033-2034	2034-2035	2035-2036	2036-2037	2037-2038	2038-2039	2039-2040	2040-2041	2041-2042	2042-2043	2043-2044	2044-2045	2045-2046	2046-2047	2047-2048	2048-2049	2049-2050	2050-2051	2051-2052	2052-2053	2053-2054	2054-2055	2055-2056	2056-2057	2057-2058	2058-2059	2059-2060	2060-2061	2061-2062	2062-2063	2063-2064	2064-2065	2065-2066	2066-2067	2067-2068	2068-2069	2069-2070	2070-2071	2071-2072	2072-2073	2073-2074	2074-2075	2075-2076	2076-2077	2077-2078	2078-2079	2079-2080	2080-2081	2081-2082	2082-2083	2083-2084	2084-2085	2085-2086	2086-2087	2087-2088	2088-2089	2089-2090	2090-2091	2091-2092	2092-2093	2093-2094	2094-2095	2095-2096	2096-2097	2097-2098	2098-2099	2099-2100	2100-2101	2101-2102	2102-2103	2103-2104	2104-2105	2105-2106	2106-2107	2107-2108	2108-2109	2109-2110	2110-2111	2111-2112	2112-2113	2113-2114	2114-2115	2115-2116	2116-2117	2117-2118	2118-2119	2119-2120	2120-2121	2121-2122	2122-2123	2123-2124	2124-2125	2125-2126	2126-2127	2127-2128	2128-2129	2129-2130	2130-2131	2131-2132	2132-2133	2133-2134	2134-2135	2135-2136	2136-2137	2137-2138	2138-2139	2139-2140	2140-2141	2141-2142	2142-2143	2143-2144	2144-2145	2145-2146	2146-2147	2147-2148	2148-2149	2149-2150	2150-2151	2151-2152	2152-2153	2153-2154	2154-2155	2155-2156	2156-2157	2157-2158	2158-2159	2159-2160	2160-2161	2161-2162	2162-2163	2163-2164	2164-2165	2165-2166	2166-2167	2167-2168	2168-2169	2169-2170	2170-2171	2171-2172	2172-2173	2173-2174	2174-2175	2175-2176	2176-2177	2177-2178	2178-2179	2179-2180	2180-2181	2181-2182	2182-2183	2183-2184	2184-2185	2185-2186	2186-2187	2187-2188	2188-2189	2189-2190	2190-2191	2191-2192	2192-2193	2193-2194	2194-2195	2195-2196	2196-2197	2197-2198	2198-2199	2199-2200	2200-2201	2201-2202	2202-2203	2203-2204	2204-2205	2205-2206	2206-2207	2207-2208	2208-2209	2209-2210	2210-2211	2211-2212	2212-2213	2213-2214	2214-2215	2215-2216	2216-2217	2217-2218	2218-2219	2219-2220	2220-2221	2221-2222	2222-2223	2223-2224	2224-2225	2225-2226	2226-2227	2227-2228	2228-2229	2229-2230	2230-2231	2231-2232	2232-2233	2233-2234	2234-2235	2235-2236	2236-2237	2237-2238	2238-2239	2239-2240	2240-2241	2241-2242	2242-2243	2243-2244	2244-2245	2245-2246	2246-2247	2247-2248	2248-2249	2249-2250	2250-2251	2251-2252	2252-2253	2253-2254	2254-2255	2255-2256	2256-2257	2257-2258	2258-2259	2259-2260	2260-2261	2261-2262	2262-2263	2263-2264	2264-2265	2265-2266	2266-2267	2267-2268	2268-2269	2269-2270	2270-2271	2271-2272	2272-2273	2273-2274	2274-2275	2275-2276	2276-2277	2277-2278	2278-2279	2279-2280	2280-2281	2281
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	1	2	3	4	5	6	7	8
A	Whole brain	Amygdala	Caudate nucleus	Cerebellum	Cerebral cortex	Frontal lobe	Hippocampus	Medulla oblongata
B	Occipital lobe	Putamen	Substantia nigra	Temporal lobe	Thalamus	Nucleus accumbens	Spinal cord	
C	Heart	Aorta	Skeletal muscle	Colon	Bladder	Uterus	Prostate	Stomach
D	Testis	Ovary	Pancreas	Pituitary gland	Adrenal gland	Thyroid gland	Salivary gland	Mammary gland
E	Kidney	Liver	Small intestine	Spleen	Thymus	Peripheral leukocyte	Lymph node	Bone marrow
F	Appendix	Lung	Trachea	Placenta				
G	Fetal brain	Fetal heart	Fetal kidney	Fetal liver	Fetal spleen	Fetal thymus	Fetal lung	
H	Yeast total RNA 100ng	Yeast tRNA 100ng	E.coli rRNA 100ng	E.coli DNA 100ng	Poly r(A) 100ng	Human Cot1 DNA 100ng	Human DNA 100ng	Human DNA 500ng

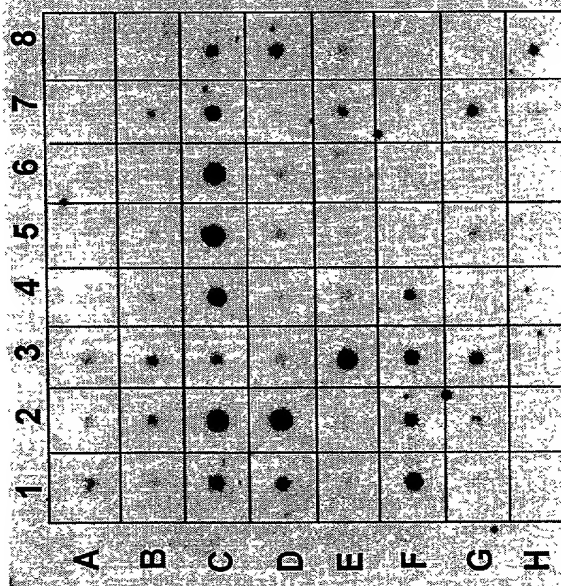


FIG. 16

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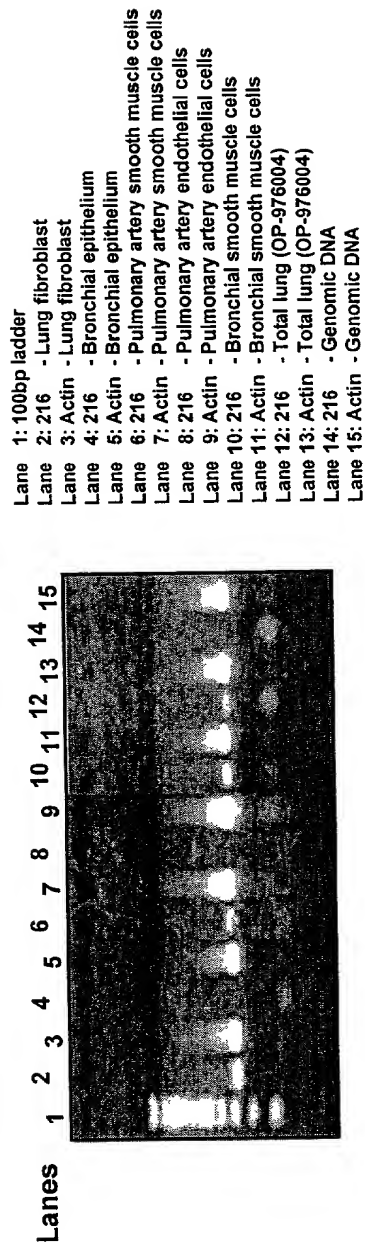


FIG. 17



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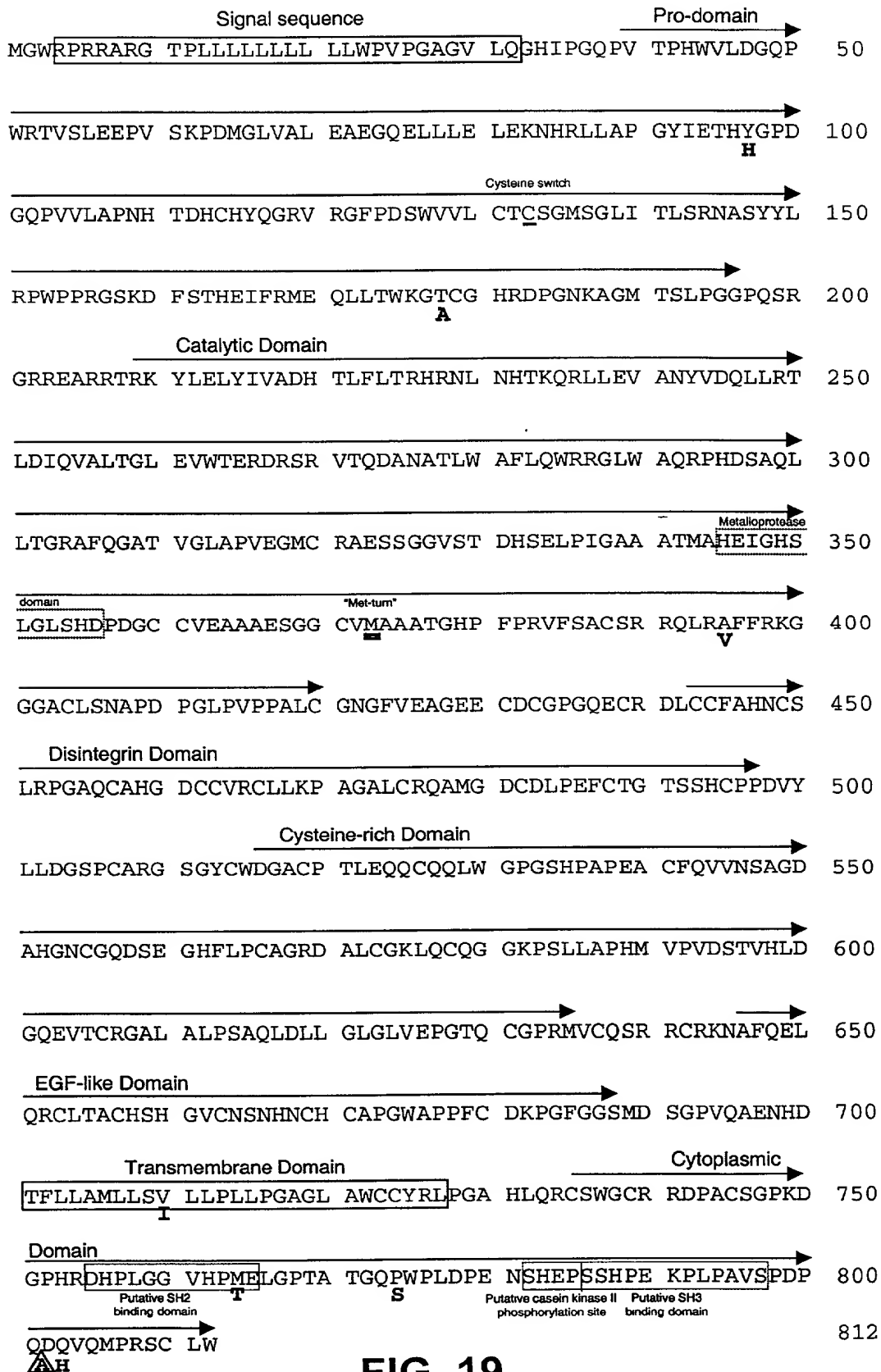


FIG. 19



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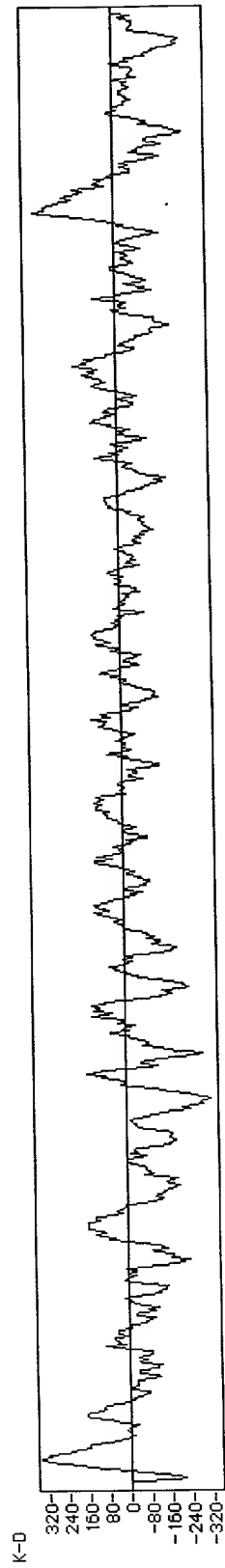
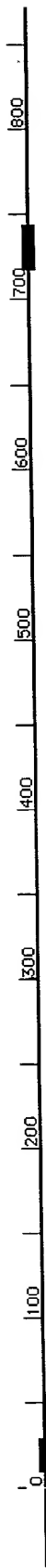


FIG. 20

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ataggttgggtaaaactcacaattgggaaaatacaaccatactccagacaaggggccaa  
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FIG. 21

cagcagcttatgtaagaaattggtagtagtggtttctgtggggaaggagtagcccaaagg  
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FIG. 21

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FIG. 21

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FIG. 21

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FIG. 21

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FIG. 21

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aattttattttatcatttgatattattttactggttagttataacaatgtgcataatatat  
gtgtaatatataaaatatataattttattatattaattattatataaatttaattatatta  
ttatacctatatatttagtacatatataggttacagaatggctacaaaagtgccagga  
gccatcaaggagaagctaaaagccagcaagtgatcttccctgagacggttctgccatggac  
tgtacaattagtgatggatttgcttctgtaggcaaggacgaggagatttcattttaggaa  
agattcctgctattaatatgcttttccctgggtattattaaatatataaacaatcactagg  
tattagcccaccgttttgaaacagaatgttctgcagaacaatgaagatgtactctcttgta  
atgatgctatatagacaaatagattatttcttttttaaaaaagaaaaagagccggcgga  
tggtggcacatgcctttaatcccagcacttgggaggcagaggcaggcagatttctgagtt  
caaggccagcctggactacagagtgagttccaggacagccagggtactcagagaaactc  
tgtcttggaaaaaaaaaaagaggaagaaagaaaaagattttattttattttatacat  
atgagtacaccatcagacacacaagaaggggcaccagaccccattacagatggttgta  
gccaccatgtggttgctgggaattgaactcaggacctctggaagaacagttggtgctctt  
aaccctgagccatctctccagcccaatagatgatttcttaattcttaaggatgatcct  
ataagaattcctaaacttacattagtaattattaagctcttttacaataggacttctatt  
aagtcttctctaatatgaaaacttcaataagaactctgccagctctcaagtgtcatgagt  
tagttgcttctgagatagcaagtaggcatcaacaacttagagcacattctaggaggttg  
aaaaccattaaccagtgggtcttaaaaagggaactaacaataggctatagggtgcaaggaca  
gaagataaaatattgactaggtttatcaatacaaaaatttaccacaaaagttatgtttt  
gacttttcataaaaactctttatgaacctgtagaactgggtgaaagatgacgaatgcttag  
ccagataattactcctaatagatatgcatgtgaatattctgtgctgtaaacttatttatg  
tttgaacttccagtgaacttttgtttaaaaaaggggggggtgaaaaagccatgtgatc  
tattctcctagaaagggtacagaagactaagaaagattacattggagatgtaaccttggg  
gagaaagctttgggagcaagagcatagagagcaaggccattgtggcatcagagcaggagg

FIG. 21



agagagcaagattagaaggagatgcagagtggaataacttagaaactataaggcaacata  
 aaaaattaagagagccatatgcagaatgcagagggaaagagaaaaaaaaaaaaaaga  
 agctgcagggagagcagaaggagcaggcaggcttctcctgaccatggggtagaacagggc  
 ttttcttaataccaaggcaggcttagtcttaaggataataaagcttttctttcttacaga  
 cttgggttttaattcatttagcaataaaaagtgtaaaagtgttttctttccctatgcaataa  
 agattggagcttatttttcagccagaatgagtgagttctctctgcaacgggtgcttgggtct  
 tttgcttcatatacacacataagtgtgtgtgtgcgcgcagtcgtgtgtgtgtgtgtgtgt  
 gtgtgtgtgtgtgtaagtgtgcaattatcagatggcatggaagctgggctcaattgggtc  
 aaatggggacttgtgagggtatatgcatgaatctgtatatgaattcatgtgagcttatat  
 atatttgcttgtgtaaaagtttttccttctgtgagtgactctcttctcctgggtcaat  
 agaggtttattgcttcaaacttccccctagcctgacagtcgagaggcatctggacaagag  
 agaaaaggetctagccattaatccttttcttagatccattttcttagagaactttcttag  
 gaaactgttttagagagaacatagaaacaggctgaaatcacttgtcaaactgtccctttt  
 ctctctaaggacttctactagcagactgggagtttagagctgcacagtccttgaggagata  
 gaacaaaggctgctttactgaatccccctgctgttttaagatgaggttctaaaggagattg  
 cagtttctgacccccaaaaggaaactcaggcaggctcagctacagtatcaaagtgacttaaa  
 cttaaagataggatagtgtttattattaaacagctaccctaaatatctcataagatcaag  
 cttaccccggtgacacttccccctctgttgctcaagaggaaccaagcagaaagaaccgc  
 cagggctggctcctggcacaatgggttaaagatgttgtagcatggggaaatgaagagat  
 ggctcagctattaagagaatatcttactcttcagaggaccagtggtcaattccagcaa  
 acatatcaggtgccacaccatcactttagctccagctgcagatctgctacatctggcct  
 ccataggcacccacacacaggtggcacccacaattaaaaaaataagataaatctaaaaca  
 gcaaagttaaagcatgagctgaaactagtaaagtgttgtgtggcatagaccaagacctg  
 ggtttggtccctacctgttagaaatagtctcagtatcacacaaaggaacacccaagcgaa  
 gcaaaagctcccagcaagacaaaactacagtcttcattgagagtgtgcacgctgaagacc  
 gagcacactgggtgcaaaatgtacttggattctgttttgcttgtttgttccagacaggggt  
 ttctctgcataaacagccttggctgtccctgaaattcactgtgttagaccaggtggcctca  
 aacctcagagatccgttcacccacgcttatctaggcttcagctctaccctgtgagatgg  
 cctgaaagtgttagaacgcgcgggatctatttctgacagactggctggcatcttttcc  
 ttctctcagcatgagattcctggggcgttcccatttcagcatcaagcatggtagcagagt  
 tggaaacctgagggctgagggctcagactcagaccataaactggaagcagagagaactgga  
 gattgtgggaggctttgaaacctcagctcctgccccagcaaataccttccagcaaggcca  
 cacctcttaaacctccccaaacaggggtaccaactggggacctaatattcaaagtccac  
 aaatatgggagacatgacatccaaaccgcccaggacaggtgtatacctccatgcttgggtt  
 ccgtagtaagaaacactaaacattagcctttcctaataaactgatataaagccctgct  
 attctcgatgtttttctctgttctgtctcctccttctccacctgcttctctgttctctga  
 cctcttctgtgtcacagatagccctgccatgtccatctgccagccatgttctgtctactt  
 gcctctctctctgtctgtgactcttctagatgcctctgggtgttctttctcatatctaca

FIG. 21

>mouse Gene 216 cDNA  
AAAGGCACTCCCAGCCTATGGGCTCGAGGTGCGGGAGACCCGGGGGGTCTCCG  
GTGCTGCTATGTCTGCCGCTGTTGCTGCCCTCGTGTCCGCTGCGGAGCGCTCG  
GATGTTTCCAGGAAATGCCCATGGAGAGCTAGTCACTCCCCACTGGATCCTGG  
AGGGCAGACTCTGGCTCAAGGTCACCCTGGAGGAGCCGATCTTGAAGCCTGAC  
TCGGTGCTGGTGGCTTTAGAGGCTGAAGGCCAGGATCTCCTGCTTGAAGTGA  
GAAGAAGCACAAAGCTTCTGGCCCCAGGATACACAGAAACCCACTACAGGCCAG  
ATGGGCATCCGGTAGTGCTGTCCCCAACACACGGATCATTGCCAATATCAC  
GGGCGTGAGGGGCTTCCGGGAATCCTGGGTGGTCTCAGCACCTGCTCTG  
GGATGAGTGGCCTTATTGTGCTCAGCAGCAAAGTCAGCTATTATCTGCAACCTC  
GGACTCCTGGGGATACCAAGACTTCCCAACCCACGAGATCTTCCGGATGGAG  
CAGTTGTTACCTGGAGAGGGGTCCAGAGAGACAAGAACTCCCAATACAAAGC  
AGGAATGGCCAGTCTTCTCATGTCCCCAGAGCCGGGTGAGGCGAGAGGCG  
CGCAGGAGTCCCAGGTACCTGGAAGTGTACATAGTGGCTGACCACACCCCTGAA  
CTTGAACACACGAGACAGCGCCTCCTGGAGGTTGCCAATTGCGTGGACCAGA  
TTCTCAGGACTCTGATATACAGTGGTGTGACCGGGCTGGAAGTGTGGACC  
GAGCAGGATCTCAGTCGCATCACTCAGGACGCAAACGAAACGCTCTGGGCTTT  
CCTACAGTGGCGCCGCGGGGTGTGGGCCAGGAGACCACGACTCCACACAA  
CTGCTCAGGGGCCGACCTTCCAGGGTACCACGGTGGGCTGGCACCTGTGG  
AGGGCATATGCCGCGCGGAGAGCTCCGGAGGTGTGAGCACAGACCACTCGGA  
ACTCCCCATCGGCACAGCAGCCACCATGGCCCACGAGATAGGCCACAGCCTGG  
GCCTCCACCATTGATCCCGAGGGCTGCTGCGTGCAGGCCGATGCAGAGCAAGG  
AGGCTGCGTCATGGAGGCGACCCACAGGGCACCCCTTTCCGCGCGTCTTCAGCG  
CCTGCAGCCGCGCCAGCTGCGCACCTTCTTCCGCAAAGGGGGCGGTCTTGC  
CTCTCCAACACCTCGGCGCCGGGGCTCCTGGTGCTGCCAGCCGCTGCGGAAA  
CGGCTTCTTGAAGCAGGAGAAGAGTGCAGTGCAGTCTGGCCAGAAGTGC  
CCGGACCCCTGCTGCTTTGCCCAAAATTGCTCCCTGCGTGCGGGGGCTCAATG  
TGCCACCGGTGATTGCTGTGCGAAGTGCCTGTTAAAGTCCGCGGGCACGCCTT  
GTCGTCCTGCTGCGACTGACTGCGATCTCCCCGAGTTCTGCACCGGCACCTCC  
CCGTATTGCCCCGCGAGATGTTTACCTACTGGATGGCTCACCTGCGCTGAGGG  
TCGCGGCTATTGCCTAGACGGCTGGTGTCCCACGCTGGAGCAGCAGTGCCAGC  
AGCTATGGGGGCTGGGTCCAAGCCGGCCCCAGAGCCATGTTTCCAGCAGAT  
GAACTCCATGGGGAATTGCAAGGGAACCTGTGCCAGGACCACAAGGGTAGC  
TTCCTGCCTTGTGCTCAGAGGGACGCTCTGTGTGGGAAACTGCTGTGCCAGGG  
AGGGGAGCCGAACCCACTAGTGCCGCACATAGTACTATGGACTCCACAATTC  
TCCTAGAGGGCCGCGAAGTGGTTTCCCGAGGGGCTTTGTGCTCCAGATAGT  
CACCTGGACAGCTTGACTTGGGTCTGGTAGAGCCAGGCACCGGCTGTGGACC  
TAGAATGGTGTGCCAGGACAGGCACTGTGAGAATGCTACCTCCAGGAGCTGG  
AACGTTGCTTGACTGCCTGCCATAACGGTGGGGTTTGCAATAGCAATCGTAAC  
GTCAGTGTGCTGCTGGCTGGGCTCCACCCTTCTGTGACAAGCCTGGCTTGGGT  
GGTAGCGTGGATAGTGGCCCTGCACAGTCTGCAACCGAGATGCCTTCCCCTT  
GGCCATGCTCCTCAGCTTCTGCTGCCTCTGCTCCCTGGGGCTGGCCTAGCCT  
GGTGCTACTACAGCTCCCAACATTCTGTCTATCGAAGGGGACTGTGCTGCAGG  
AGGGACCCCTATGGAATAGAGACATAACCCCTGGGCAGTGTGCATCCGGTGGA  
GTTTGGCTCCATCATCACTGGAGAGCCCTCGCCCCCTCCCCATGGACCTCTTG  
CCAACAGCGTTGCGACCCCTCCATCTCTTGACTTGCTCTCAGACCTGCGAACTC  
TGAGCTTACCTAAGAACTACCCCTCTGAAGCAGCCTGGTCTACAGATTGAGTTCC  
AGACCTGCCCTATCCCTATGGTATGGAAGCACCCCTGAGGACCTCCTGTTGCCA  
GTCACCTACCTCTGTCTCAGTTTGTGTCCCCTCCTCAGATTTACAGGCTTGCAT  
CAATAAAGAAATGAGACATGGGCTCAGAGAASCTGTTGTCTATAGAGACCATG  
ATGCTGGAACCCCTAGGGGAGGGAAGGGAGACACTGTGGTCTTCTTGGGTC  
CTTATAGAGGGAGGACAAATGTGCCCTGCCATGTGACTTGCACTCCTCAGTTTC  
TCAGACGCACTCTTATAATTCTATGGGCTGTATGTGAGCTCTTACTCAGCATA  
GGAACCCAGAGCCCGATCATGTTGTATCCSCCTGCCCTGAGAGCTGTGCTAT  
TCTGAAATGTAGAATGTATCTAATAACAATAAATCCACAAGTTATATCAGHAAA  
AAAAAAA

FIG. 22

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>mouse Gene 216 protein

MGSRGPRGGSPVLLLLPLLLPSCPLRSARMFPGNAHGELVTPHWILEGRLWLKVTLEEPILKPDSVLVALEAEGQDLLL  
ELEKKHKLLAPGYTETHYRPDGHVPVLSPNHTDHCQYHGRVRGFRESWVVLSTCSGMSGLIVLSSKVSYYLQPRTPGDTK  
DFPTHEIFRMEQLFTWRGVQRDKNSQYKAGMASLPHVPQSRVRREARRSPRYLELYIVADHTLNLNHTRQRLLEVANCVD  
QILRTLDIQLVLTGLEVWTEQDLSRITQDANETLWAFLOWRRGVWARRPHDSTQLLTGRTFQGTTVGLAPVEGICRAESS  
GGVSTDHSELPIGTAATMAHEIGHSLGLHHDPEGCCVQADAEQGGCVMEAATGHFFPRVFSACSRRLRTFFRKGGGPCL  
SNTSAPGLLVLPSCGNGFLEAGEECDGSGQKCPDPCFAHNCSLRAGAQCAHGDCCAKCLLKSAGTPCRPAATDCDLP  
EFCTGTSPYCPADVLLDGSPCAEGRGYCLDGWCPTLEQQCQQLWGPGSKPAPEPCFQQMNSMGNSQGNCGQDHKGSFLP  
CAQRDALCGKLLCQGGEPNPLVPHIVTMDSTILLEGREVVCRGAFVLPDSHLDQLDLGLVEPGTGCGPRMVCQDRHCQNA  
TSQELERCLTACHNGGVCNSNRNCHCAAGWAPPFCDKPGLGGSVDSGPAQSANRDAFPLAMLLSFLLPLLPAGLAWCYY  
QLPTFCHRRGLCCRRDPLWNRDIPLGSVHPVEFGSIITGEPSPPPPWTSCQQRSHPPSLDLLSDPANSELT

FIG. 22

mGene216 1 MGSRCGRPGGSPVLLLLPLLLPSCPLRSARMFPGNAHGEVTPHWILEGR 50  
 || | | | | . | | | | | | | | | | . | . | . | : | | | | : | : | .  
 hGene216 1 MGWRPRRARGTPLL LLL LLL LWPVPGAGVLQGHIPGQPVTPHWVLDGQ 49  
 . . . . .  
 mGene216 51 LWLKVTLEEPILKPDSVLVALEAEGQDLLLELEKKHKLLAPGYTETHYRP 100  
 | | | | | : | | | | | | | | | | : | | | | | | | | | |  
 hGene216 50 PWRTVSLEEPVSKPDMGLVALEAEGQELLLELEKHNHRLAPGYIETHYGP 99  
 . . . . .  
 mGene216 101 DGHPVVLSPNHT.....DHCQYHGRVGRGFRESWVVLSTCSGM 137  
 || | | | | | | | | | | | | | | : | | | | | | | | | |  
 hGene216 100 DGQPVVLAPNHTVRCFHLWDAPPEDHCHYQGRVGRGFDSWVVLCTCSGM 149  
 . . . . .  
 mGene216 138 SGLIVLSSKVSYYLQPRTPGDTKDFPTHEIFRMEQLFTWRGVQRDKNSQY 187  
 || | | | | | | | | | | | | | | : | | | | | : .  
 hGene216 150 SGLITLSRNASYLRPWPPRGSKDFSTHEIFRMEQLLTWKGTGCHRD PGN 199  
 . . . . .  
 mGene216 188 KAGMASLPHVPQSRVRREARRSPRYLELYIVADHTL.....NLNHTRQR 231  
 || | | | | | | | | | | | | | | : | | | | | | | | : | |  
 hGene216 200 KAGMTSLPGGPQSRGRREARRTRKYLELYIVADHTLFLTRHRNLNHTKQR 249  
 . . . . .  
 mGene216 232 LLEVANCVDQILRTLDIQLVLTGLEVWTEQDLSRITQDANETLWAFLOWR 281  
 || | | | | | | | | | | | | | | : | | | | | | | | | |  
 hGene216 250 LLEVANYVDQLLRTLDIQVALTGLEVWTERDRSRVTQDANATLWAFLOWR 299  
 . . . . .  
 mGene216 282 RGVWARRPHDSTQLLTGRTFQGTTVGLAPVEGICRAESSGGVSTDHSELP 331  
 || . | . | | | | | | | | | | | | | | | | | | | | | | | | | |  
 hGene216 300 RGLWAQRPHDSAQLLTGRAFAQATVGLAPVEGMCRAESSGGVSTDHSELP 349  
 . . . . .  
 mGene216 332 IGTAATMAHEIGHSLGLHHDPEGCCVQADAEQGGCVMEATGHPFPRVFS 381  
 || | | | | | | | | | | | | | | : | | | | | | | | | |  
 hGene216 350 IGAAATMAHEIGHSLGLSHDPGCCVEAAAESGGCVMAAATGHPFPRVFS 399  
 . . . . .  
 mGene216 382 ACSRRQLRTFFRKGGGPCLSN TSAPGLLVLPSCGNGFLEAGEECD CGSG 431  
 || | | | | | | | | | | | | | | | | | | | | | | | | | |  
 hGene216 400 ACSRRQLRAFFRKGGGACLSNAPDPGLPVPPALCGNGFVEAGEECD CGPG 449  
 . . . . .  
 mGene216 432 QKCPDPCCFAHNCSLRAGAQA HGDCCAKCLLKSAGTPCRPAATDCDLPE 481  
 | . | | | | | | | | | | | | | | : | | | | | | | | | |  
 hGene216 450 QECRDLCCFAHNCSLRPGAQA HGDCCVRCLLKPAGALCRQAMGDCDLPE 499  
 . . . . .  
 mGene216 482 FCTGTSPYCPADVYLLDGSPCAEGRGYCLDGWCPTLEQQCQQLWGP GSKP 531  
 || | | | | : | | | | | | | | | | | | | | | | | | | | | |  
 hGene216 500 FCTGTSSHCPPDVYLLDGSPCARGSGY CWDGACPTLEQQCQQLWGP GSHP 549  
 . . . . .  
 mGene216 532 APEPCFQQMNSMGNSQGNCGQDHKGSFLPCAQRDALCGKLLCQGGE PNPL 581  
 || | | | | . | | | | | | | | | | | | | | | | | | | | | |  
 hGene216 550 APEACFQVVNSAGDAHGNCGQDSEGHFLPCAGRDALCGKLQCQGGKPSLL 599

FIG. 23

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mGene216 582 VPHIVTMDSTILLEGREVVCRAFLPDSHLDQLDLGLVEPGTGCGPRMV 631
      |||. |. |||: |:|. | ||| | | |. | | | | | | | | | | | | | | | |
hGene216 600 APHMVPVDSTVHLDGQEVTCRGALALPSAQLDLLGLGLVEPGTQCGPRMV 649

mGene216 632 CQDRHCQNATSQELERCLTACHNGGVCNSNRNCHCAAGWAPPFCDKPGLG 681
      || | |. |||: ||| | |. | | | | | | | | | | | | | | | | | | | |
hGene216 650 CQSRRRCRKNAPQELQRCLTACHSHGVCNSNHNCHCAPGWAPPFCDKPGFG 699

mGene216 682 GSVDSGPAQSANRDAFPLAMLLSFLLPLLPGAGLAWCYQLP.TFCHRRG 730
      |||. ||| |. | | | | | | | | | | | | | | | | | | | | | | | |
hGene216 700 GSMDSGPVQAENHDTFLLAMLLSVLLPLLPGAGLAWCCYRLPGAHLQRCS 749

mGene216 731 LCCRRDPLW.....NRDIPLGSVHPVEFGSIITGEPSPPPPWTSCQQR 773
      |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
hGene216 750 WGCRRDPACSGPKDGPGRDHPLGGVHPMELGPTATGQPWPLDPENSHEPS 799

mGene216 774 SHP..PSLDLLSDPANSELT..... 791
      ||| | |. | | :.
hGene216 800 SHPEKPLPAVSPDPQADQVQMPRSCLW 826

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FIG. 23

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      10              30              50
CGGGCACGGGTCGGCCGCAATCCAGCCTGGGCGGAGCCGGAGTTGCGAGCCGCTGCCTAG
-----+-----+-----+-----+-----+-----+-----+-----+

      70              90              110
AGGCCGAGGAGCTCACAGCTATGGGCTGGAGGCCCGGAGAGCTCGGGGGACCCCGTTGC
-----+-----+-----+-----+-----+-----+-----+-----+
                      MetGlyTrpArgProArgArgAlaArgGlyThrProLeuL

      130             150             170
TGCTGCTGCTACTACTGCTGCTGCTCTGGCCAGTGCCAGGCGCCGGGGTGCTTCAAGGAC
-----+-----+-----+-----+-----+-----+-----+-----+
euLeuLeuLeuLeuLeuLeuLeuLeuTrpProValProGlyAlaGlyValLeuGlnGlyH

      190             210             230
ATATCCCTGGGCAGCCAGTCACCCCGCACTGGGTCTCTGGATGGACAACCCTGGCGCACCCG
-----+-----+-----+-----+-----+-----+-----+-----+
isIleProGlyGlnProValThrProHisTrpValLeuAspGlyGlnProTrpArgThrV

      250             270             290
TCAGCCTGGAGGAGCCGGTCTCGAAGCCAGACATGGGGCTGGTGGCCCTGGAGGCTGAAG
-----+-----+-----+-----+-----+-----+-----+-----+
alSerLeuGluGluProValSerLysProAspMetGlyLeuValAlaLeuGluAlaGluG

      310             330             350
GCCAGGAGCTCCTGCTTGAGCTGGAGAAGAACCACAGGCTGCTGGCCCCAGGATACATAG
-----+-----+-----+-----+-----+-----+-----+-----+
lyGlnGluLeuLeuLeuGluLeuGluLysAsnHisArgLeuLeuAlaProGlyTyrIleG

      370             390             410
AAACCCACTACGGCCAGATGGGCAGCCAGTGGTGCTGGCCCCCAACCACACGGTGAGAT
-----+-----+-----+-----+-----+-----+-----+-----+
luThrHisTyrGlyProAspGlyGlnProValValLeuAlaProAsnHisThrValArgC

      430             450             470
GCTTCCATGGGCTCTGGGATGCACCGCCAGAGGATCATTGCCACTACCAAGGGCGAGTAA
-----+-----+-----+-----+-----+-----+-----+-----+
ysPheHisGlyLeuTrpAspAlaProProGluAspHisCysHisTyrGlnGlyArgValA

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FIG. 24

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      490              510              530
      .               .               .
GGGGCTTCCCCGACTCCTGGGTAGTCCTCTGCACCTGCTCTGGGATGAGTGGCCTGATCA
-----+-----+-----+-----+-----+-----+-----+
rgGlyPheProAspSerTrpValValLeuCysThrCysSerGlyMetSerGlyLeuIleT

      550              570              590
      .               .               .
CCCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGACT
-----+-----+-----+-----+-----+-----+-----+
hrLeuSerArgAsnAlaSerTyrTyrLeuArgProTrpProProArgGlySerLysAspP

      610              630              650
      .               .               .
TCTCAACCCACGAGATCTTTTCGGATGGAGCAGCTGCTCACCTGGAAGGAACCTGTGGCC
-----+-----+-----+-----+-----+-----+-----+
heSerThrHisGluIlePheArgMetGluGlnLeuLeuThrTrpLysGlyThrCysGlyH

      670              690              710
      .               .               .
ACAGGGATCCTGGGAACAAAGCGGGCATGACCAGCCTTCCTGGTGGTCCCCAGAGCAGGG
-----+-----+-----+-----+-----+-----+-----+
isArgAspProGlyAsnLysAlaGlyMetThrSerLeuProGlyGlyProGlnSerArgG

      730              750              770
      .               .               .
GCAGGCGAGAAGCGCGCAGGACCCGGAAGTACCTGGAAGTGTACATTGTGGCAGACCACA
-----+-----+-----+-----+-----+-----+-----+
lyArgArgGluAlaArgArgThrArgLysTyrLeuGluLeuTyrIleValAlaAspHist

      790              810              830
      .               .               .
CCCTGTTCTTGACTCGGCACCGAAACTTGAACCACACCAAACAGCGTCTCCTGGAAGTCG
-----+-----+-----+-----+-----+-----+-----+
hrLeuPheLeuThrArgHisArgAsnLeuAsnHisThrLysGlnArgLeuLeuGluValA

      850              870              890
      .               .               .
CCAACCTACGTGGACCAGCTTCTCAGGACTCTGGACATTCAAGGTGGCGCTGACCGGCCTGG
-----+-----+-----+-----+-----+-----+-----+
laAsnTyrValAspGlnLeuLeuArgThrLeuAspIleGlnValAlaLeuThrGlyLeuG

      910              930              950
      .               .               .
AGGTGTGGACCGAGCGGGACCGCAGCCGCGTCACGCAGGACGCCAACGCCACGCTCTGGG
-----+-----+-----+-----+-----+-----+-----+
luValTrpThrGluArgAspArgSerArgValThrGlnAspAlaAsnAlaThrLeuTrpA

      970              990             1010

```

FIG. 24

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CCTTCCTGCAGTGGCGCCGGGGCTGTGGGCGCAGCGGCCCCACGACTCCGCGCAGCTGC
-----+-----+-----+-----+-----+-----+
laPheLeuGlnTrpArgArgGlyLeuTrpAlaGlnArgProHisAspSerAlaGlnLeuL

      1030              1050              1070
TCACGGGCCGCGCCTTCCAGGGCGCCACAGTGGGCCTGGCGCCCGTCGAGGGCATGTGCC
-----+-----+-----+-----+-----+-----+
euThrGlyArgAlaPheGlnGlyAlaThrValGlyLeuAlaProValGluGlyMetCysA

      1090              1110              1130
GCGCCGAGAGCTCGGGAGGCGTGAGCACGGACCACTCGGAGCTCCCCATCGGCGCCCGCAG
-----+-----+-----+-----+-----+-----+
rgAlaGluSerSerGlyGlyValSerThrAspHisSerGluLeuProIleGlyAlaAlaA

      1150              1170              1190
CCACCATGGCCCATGAGATCGGCCACAGCCTCGGCCTCAGCCACGACCCCGACGGCTGCT
-----+-----+-----+-----+-----+-----+
laThrMetAlaHisGluIleGlyHisSerLeuGlyLeuSerHisAspProAspGlyCysC

      1210              1230              1250
GCGTGAGGCTGCGGCCGAGTCCGGAGGCTGCGTCATGGCTGCGGCCACCGGGCACCCGT
-----+-----+-----+-----+-----+-----+
ysValGluAlaAlaAlaGluSerGlyGlyCysValMetAlaAlaAlaThrGlyHisProp

      1270              1290              1310
TTCCGCGCGTGTTCAGCGCCTGCAGCCGCCGAGCTGCGCGCTTCTTCCGCAAGGGGG
-----+-----+-----+-----+-----+-----+
heProArgValPheSerAlaCysSerArgArgGlnLeuArgAlaPhePheArgLysGlyG

      1330              1350              1370
GCGGCGCTTGCCCTCTCCAATGCCCCGGACCCCGGACTCCCGGTGCCGCCGGCGCTCTGCG
-----+-----+-----+-----+-----+-----+
lyGlyAlaCysLeuSerAsnAlaProAspProGlyLeuProValProProAlaLeuCysG

      1390              1410              1430
GGAACGGCTTCGTGGAAGCGGGCGAGGAGTGTGACTGCGGCCCTGGCCAGGAGTGCCGCG
-----+-----+-----+-----+-----+-----+
lyAsnGlyPheValGluAlaGlyGluGluCysAspCysGlyProGlyGlnGluCysArgA

      1450              1470              1490

```

FIG. 24



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ACCTCTGCTGCTTTGCTCACAACCTGCTCGCTGCGCCCGGGGGCCAGTGCGCCACGGGG  
-----+-----+-----+-----+-----+-----+  
spLeuCysCysPheAlaHisAsnCysSerLeuArgProGlyAlaGlnCysAlaHisGlyA

1510 1530 1550  
ACTGTGCGTGCGCTGCCTGCTGAAGCCGGCTGGAGCGCTGTGCCGCCAGGCCATGGGTG  
-----+-----+-----+-----+-----+-----+  
spCysCysValArgCysLeuLeuLysProAlaGlyAlaLeuCysArgGlnAlaMetGlyA

1570 1590 1610  
ACTGTGACCTCCCTGAGTTTGCACGGGCACCTCCTCCCAGTGTCCCCAGACGTTTACC  
-----+-----+-----+-----+-----+-----+  
spCysAspLeuProGluPheCysThrGlyThrSerSerHisCysProProAspValTyrL

1630 1650 1670  
TACTGGACGGCTCACCTGTGCCAGGGGCAGTGGCTACTGCTGGGATGGCGCATGTCCCA  
-----+-----+-----+-----+-----+-----+  
euLeuAspGlySerProCysAlaArgGlySerGlyTyrCysTrpAspGlyAlaCysProT

1690 1710 1730  
CGCTGGAGCAGCAGTGCCAGCAGCTCTGGGGGCCTGGCTCCCACCCAGCTCCCGAGGCCT  
-----+-----+-----+-----+-----+-----+  
hrLeuGluGlnGlnCysGlnGlnLeuTrpGlyProGlySerHisProAlaProGluAlaC

1750 1770 1790  
GTTTCCAGGTGGTGAACCTCTGCGGGAGATGCTCATGGAACTGCGGCCAGGACAGCGAGG  
-----+-----+-----+-----+-----+-----+  
ysPheGlnValValAsnSerAlaGlyAspAlaHisGlyAsnCysGlyGlnAspSerGluG

1810 1830 1850  
GCCACTTCCTGCCCTGTGCAGGGAGGGATGCCCTGTGTGGGAAGCTGCAGTGCCAGGGTG  
-----+-----+-----+-----+-----+-----+  
lyHisPheLeuProCysAlaGlyArgAspAlaLeuCysGlyLysLeuGlnCysGlnGlyG

1870 1890 1910  
GAAAGCCCAGCCTGCTCGCACCGCACATGGTGCCAGTGGACTCTACCGTTACCTAGATG  
-----+-----+-----+-----+-----+-----+  
lyLysProSerLeuLeuAlaProHisMetValProValAspSerThrValHisLeuAspG

1930 1950 1970  
GCCAGGAAGTGACTTGTGCGGGAGCCTTGGCACTCCCCAGTGCCAGCTGGACCTGCTTG

FIG. 24

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```

-----+-----+-----+-----+-----+-----+
lyGlnGluValThrCysArgGlyAlaLeuAlaLeuProSerAlaGlnLeuAspLeuLeuG

      1990              2010              2030
      .               .               .
GCCTGGGCGCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAATGGTGTGCCAGAGCAGGC
-----+-----+-----+-----+-----+
lyLeuGlyLeuValGluProGlyThrGlnCysGlyProArgMetValCysGlnSerArgA

      2050              2070              2090
      .               .               .
GCTGCAGGAAGAATGCCTTCCAGGAGCTTCAGCGCTGCCTGACTGCCTGCCACAGCCACG
-----+-----+-----+-----+-----+
rgCysArgLysAsnAlaPheGlnGluLeuGlnArgCysLeuThrAlaCysHisSerHisG

      2110              2130              2150
      .               .               .
GGGTTTGCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCCACCCTTCTGTG
-----+-----+-----+-----+-----+
lyValCysAsnSerAsnHisAsnCysHisCysAlaProGlyTrpAlaProProPheCysA

      2170              2190              2210
      .               .               .
ACAAGCCAGGCTTTGGTGGCAGCATGGACAGTGGCCCTGTGCAGGCTGAAAACCATGACA
-----+-----+-----+-----+-----+
spLysProGlyPheGlyGlySerMetAspSerGlyProValGlnAlaGluAsnHisAspT

      2230              2250              2270
      .               .               .
CCTTCCTGCTGGCCATGCTCCTCAGCGTCCTGCTGCCTCTGCTCCCAGGGGCCCGCCTGG
-----+-----+-----+-----+-----+
hrPheLeuLeuAlaMetLeuLeuSerValLeuLeuProLeuLeuProGlyAlaGlyLeuA

      2290              2310              2330
      .               .               .
CCTGGTGTGCTACCGACTCCCAGGAGCCCATCTGCAGCGATGCAGCTGGGGCTGCAGAA
-----+-----+-----+-----+-----+
laTrpCysCysTyrArgLeuProGlyAlaHisLeuGlnArgCysSerTrpGlyCysArgA

      2350              2370              2390
      .               .               .
GGGACCCTGCGTGTCAGTGGCCCCAAAGATGGCCCACACAGGGACCACCCCCTGGGCGGCG
-----+-----+-----+-----+-----+
rgAspProAlaCysSerGlyProLysAspGlyProHisArgAspHisProLeuGlyGlyV

      2410              2430              2450
      .               .               .
TTCACCCCATGGAGTTGGGCCCCACAGCCACTGGACAGCCCTGGCCCCTGGACCCTGAGA
-----+-----+-----+-----+-----+

```

FIG. 24

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alHisProMetGluLeuGlyProThrAlaThrGlyGlnProTrpProLeuAspProGluA

2470 2490 2510  
 ACTCTCATGAGCCCAGCAGCCACCCTGAGAAGCCTCTGCCAGCAGTCTCGCCTGACCCCC  
 -----+-----+-----+-----+-----+  
 snSerHisGluProSerSerHisProGluLysProLeuProAlaValSerProAspProG

2530 2550 2570  
 AAGCAGATCAAGTCCAGATGCCAAGATCCTGCCTCTGGTGAGAGGTAGCTCCTAAAATGA  
 -----+-----+-----+-----+-----+  
 lnAlaAspGlnValGlnMetProArgSerCysLeuTrpEnd

2590 2610 2630  
 ACAGATTTAAAGACAGGTGGCCACTGACAGCCACTCCAGGAAGTTGAAGTGCAGGGGCAG  
 -----+-----+-----+-----+-----+  
 -----+-----+-----+-----+-----+

2650 2670 2690  
 AGCCAGTGAATCACCGGACCTCCAGCACCTGCAGGCAGCTTGAAGTTTCTTCCCCGAGT  
 -----+-----+-----+-----+-----+  
 -----+-----+-----+-----+-----+

2710 2730 2750  
 GGAGCTTCGACCCACCCACTCCAGGAACCCAGAGCCACATAGAAAGTTCTGAGGGCTGG  
 -----+-----+-----+-----+-----+  
 -----+-----+-----+-----+-----+

2770 2790 2810  
 AGAACACTGCTGGGCACACTCTCCAGCTCAATAAACCATCAGTCCCAGAAGCAAAGGTCA  
 -----+-----+-----+-----+-----+  
 -----+-----+-----+-----+-----+

2830 2850 2870  
 CACAGCCCCTGACCTCCCTCACCAGTGGAGGCTGGGTAGTGCTGGCCATCCCAAAGGGC  
 -----+-----+-----+-----+-----+  
 -----+-----+-----+-----+-----+

2890 2910 2930  
 TCTGTCTCTGGGAGTCTGGTGTGTCTCTACATGCAATTCCACGGACCCAGCTCTGTGGA  
 -----+-----+-----+-----+-----+  
 -----+-----+-----+-----+-----+

2950 2970 2990  
 GGGCATGACTGCTGGCCAGAAGCTAGTGGTCCTGGGGCCCTATGGTTCGACTGAGTCCAC  
 -----+-----+-----+-----+-----+  
 -----+-----+-----+-----+-----+

FIG. 24

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```

      3010              3030              3050
ACTCCCCTGCAGCCTGGCTGGCCTCTGCAAACAAACATAATTTTGGGGACCTTCCTTCCT
-----+-----+-----+-----+-----+-----+-----+

      3070              3090              3110
GTTTCTTCCCACCCTGTCTTCTCCCCTAGGTGGTTCCTGAGCCCCACCCCAATCCCAG
-----+-----+-----+-----+-----+-----+-----+

      3130              3150              3170
TGCTACACCTGAGGTTCTGGAGCTCAGAATCTGACAGCCTCTCCCCCATTCTGTGTGTGT
-----+-----+-----+-----+-----+-----+-----+

      3190              3210              3230
CGGGGGGACAGAGGGAACCATTTAAGAAAAGATACCAAAGTAGAAGTCAAAGAAAGACA
-----+-----+-----+-----+-----+-----+-----+

      3250              3270              3290
TGTTGGCTATAGGCGTGGTGGCTCATGCCCTATAATCCAGCACTTTGGGAAGCCGGGGTA
-----+-----+-----+-----+-----+-----+-----+

      3310              3330              3350
GGAGGATCACCAGAGGCCAGCAGGTCCACACCAGCCTGGGCAACACAGCAAGACACCGCA
-----+-----+-----+-----+-----+-----+-----+

      3370              3390              3410
TCTACAGAAAAAATTTTAAAAATTAGCTGGGCGTGGTGGTGTGTACCTGTAGGCCTAGCTGC
-----+-----+-----+-----+-----+-----+-----+

      3430              3450              3470
TCAGGAGGCTGAAGCAGGAGGATCACTTGAGCCTGAGTTCAACACTGCAGTGAGCTATGG
-----+-----+-----+-----+-----+-----+-----+

      3490              3510              3530
TGGCACCCTGCACTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCTAAAAATAAATTTT
-----+-----+-----+-----+-----+-----+-----+

      3550              3570              3590

```

FIG. 24

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AAAAAGACATAAA  
-----+-----+-----+-----+-----+-----+

3610

AAAAAAAAAAAAAAAAAAAAAAAAA  
-----+-----+

FIG. 24

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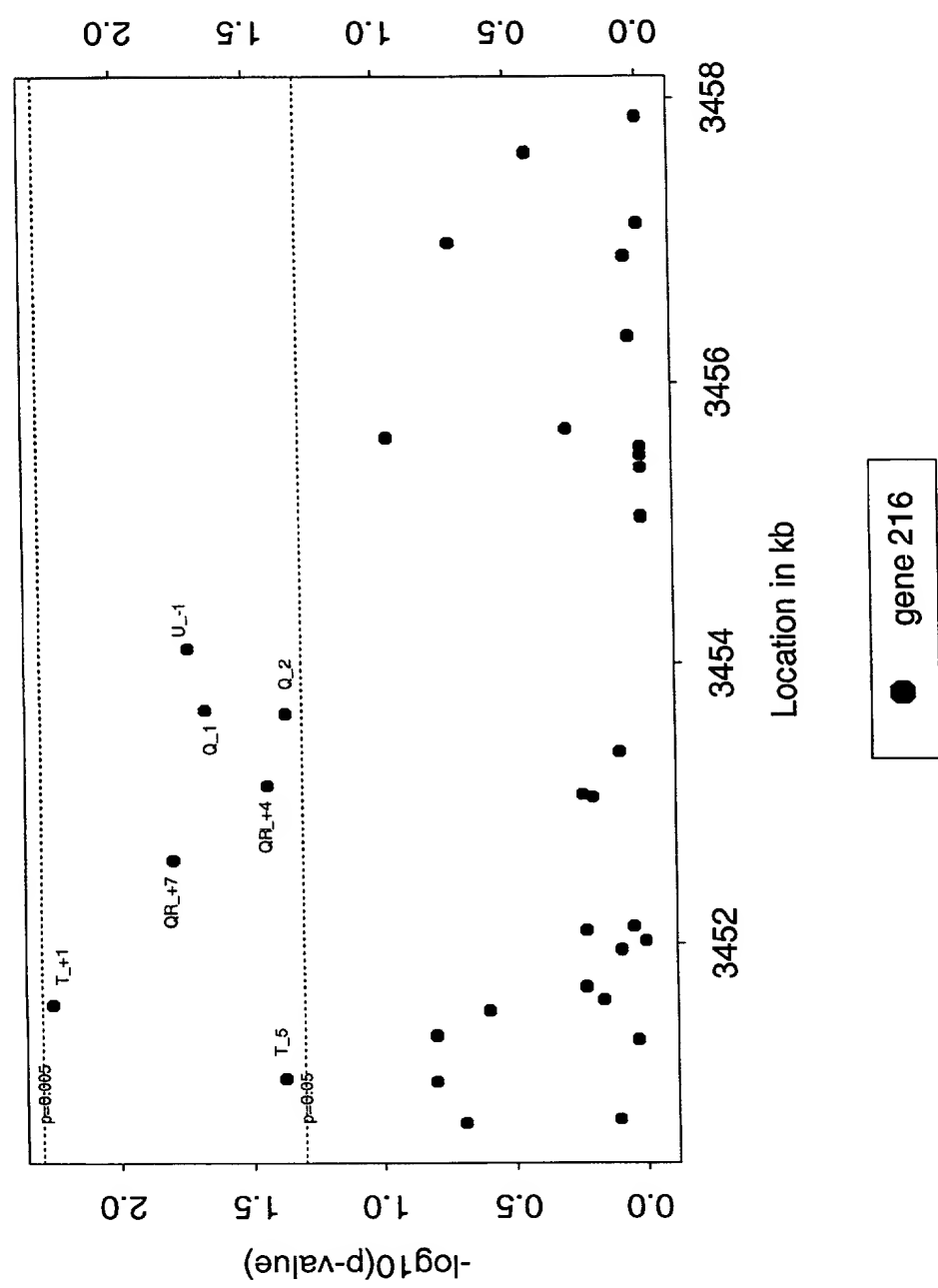


FIG. 25

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US

UK

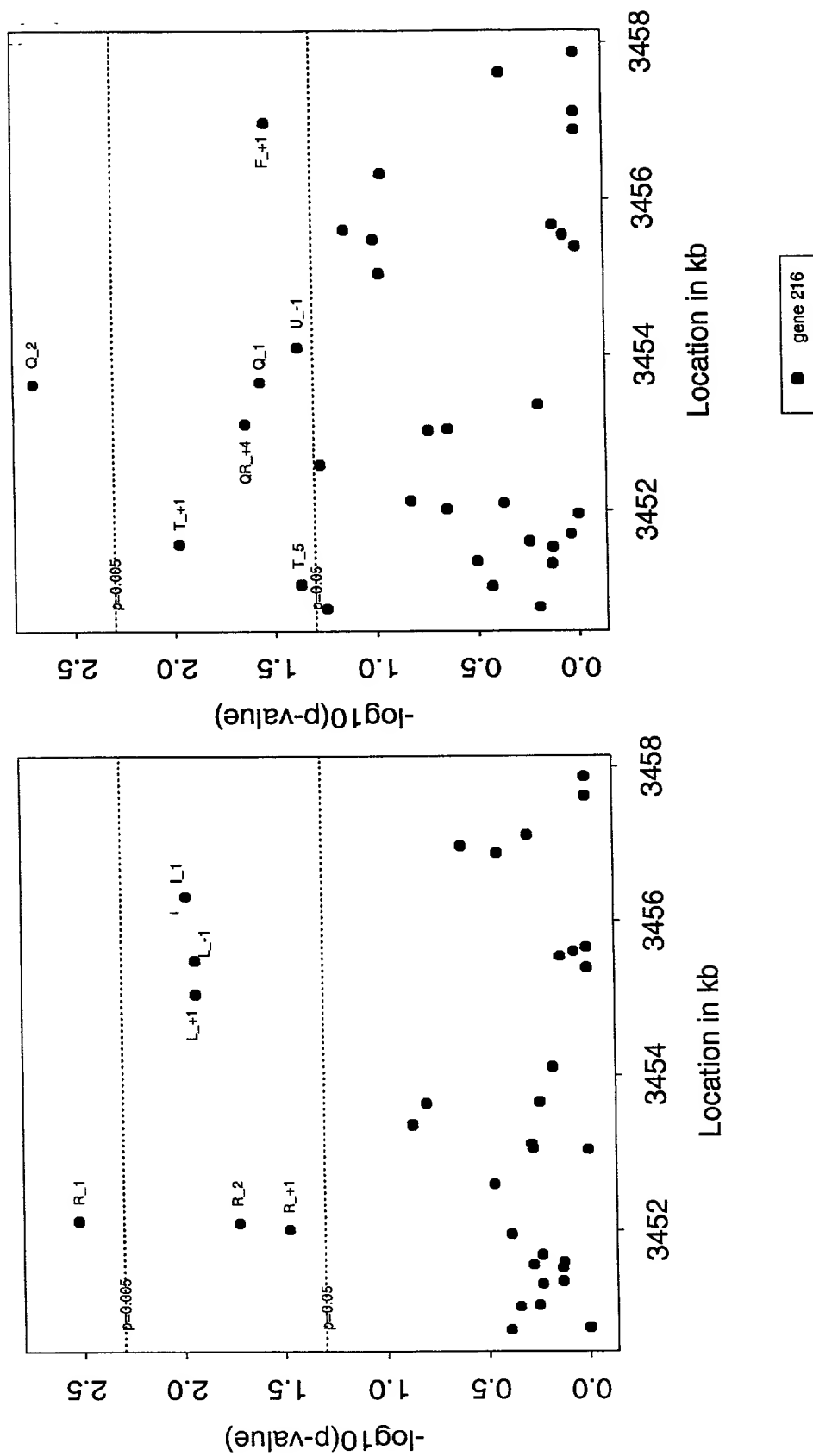


FIG. 26

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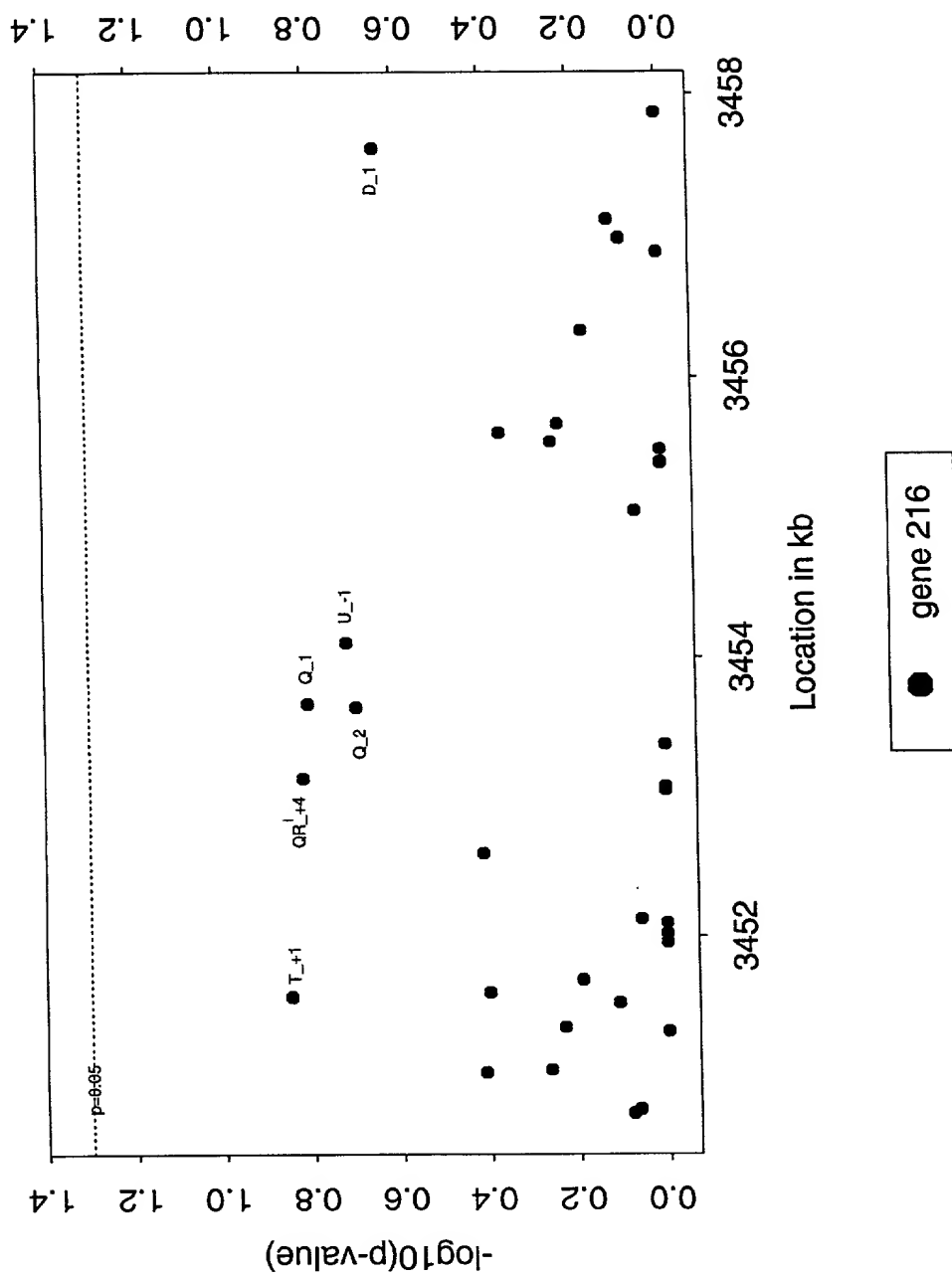


FIG. 27



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US

UK

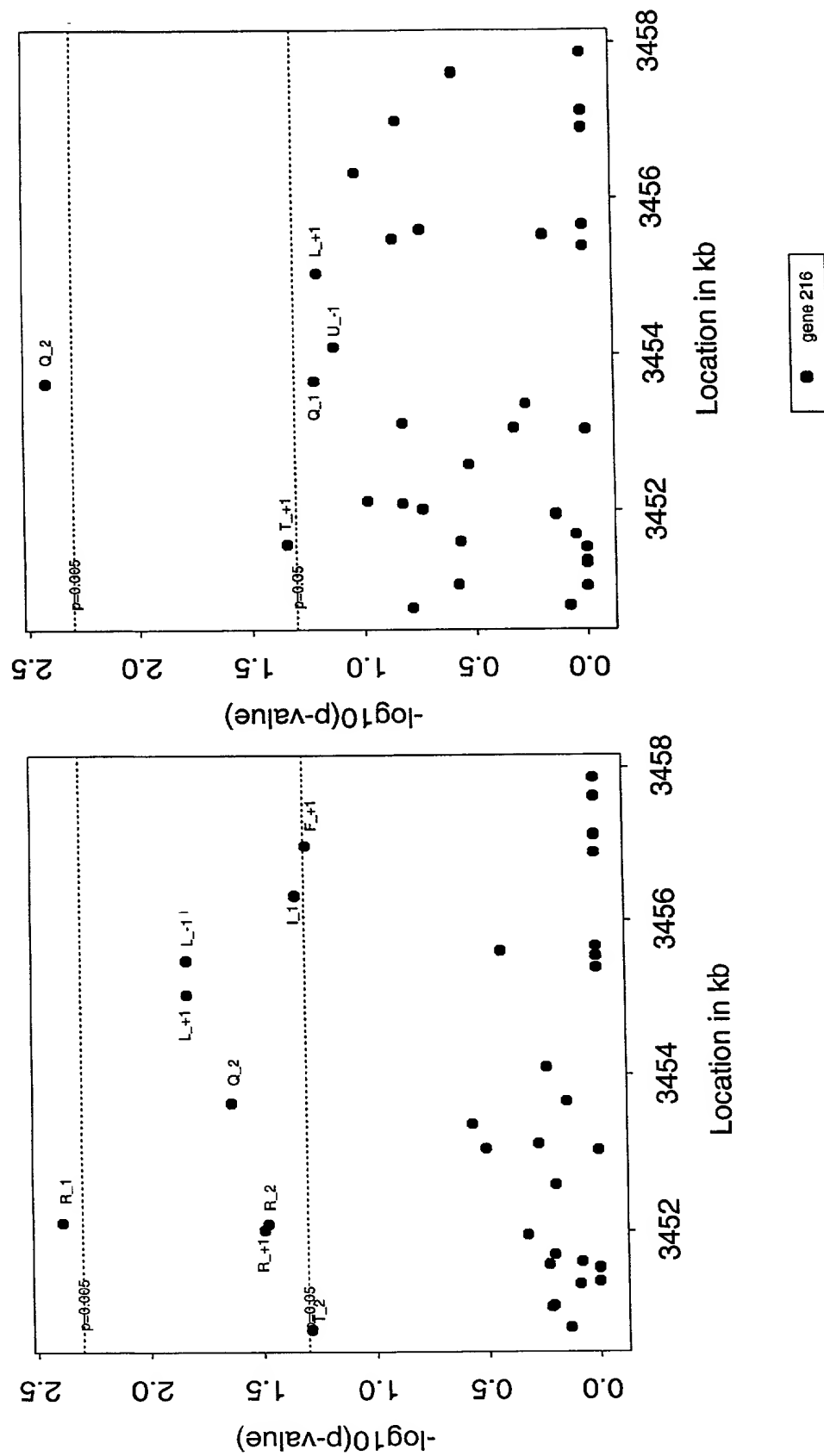


FIG. 28



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GCTTCCAGTGGTCTGAGGCCTCCTGAGACTTTTTGTACATTCAATTAAAGTGTAACATAC  
-----+-----+-----+-----+-----+-----+  
610 630 650  
AGAAAAGTTCACACATTATAAATGCAACTCAAGGACTTTTCCAAAAGCGAACACACCCAG  
-----+-----+-----+-----+-----+-----+  
670 690 710  
ATCAAGAAATAGACCATCCTACAGTCCCCCTTACACTCTGTACCAGTTGCAGCCCCAC  
-----+-----+-----+-----+-----+-----+  
730 750 770  
AAGGGTAACTACTGTCTTGACTTCGAACACCATAGATTGATTTGCCTGTTTTTAAACTT  
-----+-----+-----+-----+-----+-----+  
790 810 830  
TACATAAGTAGAATCACAGAGTGTGTACAATGACTTTGGAAAAGTGTGACAATATCTA  
-----+-----+-----+-----+-----+-----+  
850 870 890  
TTAAAGCTAAAATACCCTTGCCCTATGAACCTGAAATTCCACCCACCTTGCCAAGGGACA  
-----+-----+-----+-----+-----+-----+  
910 930 950  
AAAAGTTCCTCTCTAAATGCACCAGGCTGTGAGGATGAAGCGTTGGCTTTGGGGCCCCC  
-----+-----+-----+-----+-----+-----+  
970 990 1010  
ATTACACACATGACCTTTTCTGGGGCACCAAGCATCAGCCTGTCGTCACCAGGTGCCA  
-----+-----+-----+-----+-----+-----+  
1030 1050 1070  
CCCTGGCGATCTCTGAAGGCTGGAGTCGGAGTGCCTCCCTCAGACATCCTGTTCTGCGTC  
-----+-----+-----+-----+-----+-----+  
1090 1110 1130  
ACTCCTTGGGAGAAGTCGTGTTTACAGATGGTGGGTGTCACCCATGCCAAGCACTTCTAA  
-----+-----+-----+-----+-----+-----+

FIG. 29

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1150 1170 1190  
GGGTTAATGCTCACTGGTTTGCCTGGTTCCCAGGACATTTCTGATGCCCCTCTGGAGGG  
-----+-----+-----+-----+-----+-----+-----+  
1210 1230 1250  
TGACGCCAACAAAGCCAGTGGAGAAGCCATCTTTCCCAGGTGCTGTCAGGCGCCCCGGAG  
-----+-----+-----+-----+-----+-----+-----+  
1270 1290 1310  
CTGCTCGGTGCATCCTAGGATCCCTCTTCCTCAGCTTTGGTTTGATGGCCTCATCTCCTC  
-----+-----+-----+-----+-----+-----+-----+  
1330 1350 1370  
CCCTGCAACCTCAAAATGTAAATAAACCTTTCTCAGAGACTTCGGCAGAAAATTCCTCT  
-----+-----+-----+-----+-----+-----+-----+  
1390 1410 1430  
GACCTGCACTTGGACACAGCTCATCTGGGTTTGGGAGGTGCAACTGTGTAAGGATGACT  
-----+-----+-----+-----+-----+-----+-----+  
1450 1470 1490  
CTGATCCCCATGTGGCTTTTCGACTGTGTCCCCTCTACAGTCAGTTATTAGCACTGACTG  
-----+-----+-----+-----+-----+-----+-----+  
1510 1530 1550  
TGCTAGGAAGTGAGCAACACACATATTCCCAGACCACATGGAGCTCAGGAGCTTGGGGAG  
-----+-----+-----+-----+-----+-----+-----+  
1570 1590 1610  
AGAGACAGGGAAGTGGACGACTACAGGGCCTTCTGAAACGTGTTGCAGGGAGAAGTGTCA  
-----+-----+-----+-----+-----+-----+-----+  
1630 1650 1670  
GTCAGGGGATGCTAACCTGGCTTTGGGTAAGGGACAGCCTCTGAATGACAGGACATTAAA  
-----+-----+-----+-----+-----+-----+-----+  
1690 1710 1730

FIG. 29

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GCCATGGCCTGCAGTTTAAGTAGGAGTTGGCCAGTTCGAGGTAAGAATACCAGTAAGCAA  
-----+-----+-----+-----+-----+-----+-----+

1750 1770 1790  
GAACGCCAGAGTAGCTCCTCGAGCTGCCTTCTGTACCTGACATCCACACTGAAGCCAGCC  
-----+-----+-----+-----+-----+-----+-----+

1810 1830 1850  
CCTCTGTGTTTCAGCCTTGCTTTACTGAAGAGGTGTCGCTGAGGGGCTGCTCTGGGGTGCT  
-----+-----+-----+-----+-----+-----+-----+

1870 1890 1910  
GCTCTGCTTTTCTGTCCCCAACTTGTTCTGAGCTCGAGCCACCTCCATACTGGTGCTCCT  
-----+-----+-----+-----+-----+-----+-----+

1930 1950 1970  
GGTTCTCAGGCCTTTGAACTCAAACCTGAATCACACCACTGGCTTTCCTCGTTCTCCAGCT  
-----+-----+-----+-----+-----+-----+-----+

1990 2010 2030  
TGCAGATGGCAGATTTCGGGAACTTTTTGGCCTCCATAATCACGTGAGCCAATTGCTATAA  
-----+-----+-----+-----+-----+-----+-----+

2050 2070 2090  
TAAATATCTCTCTCCCTCTTTCTTCTCTCTCTCTCTCTGTGCAAATATAGTTCCAATTA  
-----+-----+-----+-----+-----+-----+-----+

2110 2130 2150  
TAAGAGCCCCTAACTGGAAAATAACCTATGGTGCACTGGTGAGTAGAGAACTGTGGTT  
-----+-----+-----+-----+-----+-----+-----+

2170 2190 2210  
CCCTCAAACCACCGAACACTATTCAGCAATACGAAGGAACAACTATTGATATGCAAAA  
-----+-----+-----+-----+-----+-----+-----+

2230 2250 2270  
AGTGTAATGAATCTCAAAAACATCGGAAAGAGGGAAGGAAGCCAGACACAGAAGAGTGC  
-----+-----+-----+-----+-----+-----+-----+

FIG. 29

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```

2290                2310                2330
ATGCCGCATGATTCCATTTATATGAAATTCTAGAACAGGCAAACTTATCTATAGACAGA
-----+-----+-----+-----+-----+-----+-----+

2350                2370                2390
GAACAACAGATCAGTGGCTGTCTGGGGTTGGGAGTGGGGAAGTTTGGCTGGAAGGGCACAA
-----+-----+-----+-----+-----+-----+-----+

2410                2430                2450
GGGCTCTTTCTGTGAGTGAGGGAATGTGTCTGCATTATAGTGATGCTTATGTAGTTATAT
-----+-----+-----+-----+-----+-----+-----+

2470                2490                2510
ACACTTATCGAAACTCATCTTACTGGCCACTTAAAATAAGTGCATTTTATTGTGTGTAA
-----+-----+-----+-----+-----+-----+-----+

2530                2550                2570
TTATACCTTAATGAAGTTGATTTGAAAATCCAAAGTAGTAATAATAAGTAATAATCTCGT
-----+-----+-----+-----+-----+-----+-----+

2590                2610                2630
AGCTGGACAGCTGTGGTGACTCACTCCTGTAATTCCAGCGATTTGAGAAGCTGAGGCAGG
-----+-----+-----+-----+-----+-----+-----+

2650                2670                2690
AGGATCACTTAAGATCAGGAGTTCTTTTTATTTTATTTTATTTTATTTTGGAGACGGAGTT
-----+-----+-----+-----+-----+-----+-----+

2710                2730                2750
CGCTCTTGTGCCCAGGCTGGAGTGCAATGGCATGATCTCGGCTCGCTGCAACCTCCACC
-----+-----+-----+-----+-----+-----+-----+

2770                2790                2810
TTCTGAGTTCAAGCGATTTTCCTGCCTCAGCCTCCCAAGTAGCTGGAACCTACAGGCGCTC
-----+-----+-----+-----+-----+-----+-----+

2830                2850                2870

```

FIG. 29

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```
ACCACCATGCCCGGCTAATTTTGTATTTTAGTAGAGATGGGGTTTCACCATGTTGGCC
-----+-----+-----+-----+-----+-----+-----+
2890                2910                2930
AGACTGGTCTTGAACCTCTGACCTCCAGTGATCTGCCCGCCTCGGCCTCCCAAAGTGCTG
-----+-----+-----+-----+-----+-----+-----+
2950                2970                2990
GGATTACAGGCATGAGACACTGCGCCTGGCCAAGACCAGGAGTTTGAGACCAGCCTGGGA
-----+-----+-----+-----+-----+-----+-----+
3010                3030                3050
AACAAAGTGAGACCCCCTGTCTACAGAAAAATTAAAAATTTAGCTGGGCCTGGTGCCGT
-----+-----+-----+-----+-----+-----+-----+
3070                3090                3110
GTGCCTGTAGTTCCAGCTACTCAGGAGGCTGAGGTGGGAGGATACCTTGAGCCCAGGATT
-----+-----+-----+-----+-----+-----+-----+
3130                3150                3170
TCAAGGCTGCAATGAGGCATGATCAGGCCACTGTCCTCTAGCGTGGGTGACAGAGTGAGA
-----+-----+-----+-----+-----+-----+-----+
3190                3210                3230
CCCTGTCTCTAAATAATAATCATAAGAACAACAAGGACCCCTCTAAACGCACTGATATCTA
-----+-----+-----+-----+-----+-----+-----+
3250                3270                3290
AGGTGTATTAAGCGACCAAAAAAAAAAAGAAAATCAAAGTGACAGAAAAACGTTAATAAGA
-----+-----+-----+-----+-----+-----+-----+
3310                3330                3350
GAAAAAATATGTCTGTATGTCTTGAGTGTGAAAAATAATCTAAAAGCCTATGAAAGA
-----+-----+-----+-----+-----+-----+-----+
3370                3390                3410
AACTAATCATATTGGTTTCCTGTTGGTGAGGAGGGCTAAGAGCACGGAGACTTTTCCCTA
-----+-----+-----+-----+-----+-----+-----+
```

FIG. 29

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```
3430          3450          3470
      .      .      .      .      .      .
TGCTTTCTGTACTTTTTGATTTTGAGATATGTGAATGTAGGTTTCTCTCACTGCTCGAAC
-----+-----+-----+-----+-----+-----+-----+

3490          3510          3530
      .      .      .      .      .      .
TTTCACTAACCAAATTACTACATTCCAAATTCTCAAAAACAAATAGATTTACTTAAAAGT
-----+-----+-----+-----+-----+-----+-----+

3550          3570          3590
      .      .      .      .      .      .
AGGCTGGGTGCGGTGTCTCACGCCTGTAATTCCAGCGCTTTGGGAGGCCGAGGCGGGCAG
-----+-----+-----+-----+-----+-----+-----+

3610          3630          3650
      .      .      .      .      .      .
ATCACCTGAGGTCTGGGAGTTCGAGACCAGCCTGACCAACATGGAGAAACCCATCTCTAC
-----+-----+-----+-----+-----+-----+-----+

3670          3690          3710
      .      .      .      .      .      .
TAAAAATACAAAATTAGCCAGGCGTGGTGGCGAATGCCTGTAATGCCAGCTACTCGGGAG
-----+-----+-----+-----+-----+-----+-----+

3730          3750          3770
      .      .      .      .      .      .
GCTGAGGCAGAAGAATCACTTGAATCTGGGAGGCAGAGGTTGCAGTGAGCCCAGATCATG
-----+-----+-----+-----+-----+-----+-----+

3790          3810          3830
      .      .      .      .      .      .
CCATTGCACTCCAGTCTGGGTAACAAGAGAGAACTCTGTCTCAAAAAAAAAAAAAAAAAA
-----+-----+-----+-----+-----+-----+-----+

3850          3870          3890
      .      .      .      .      .      .
AAAAGATTTGCTTAAAAGTTAACATCTCCGGCCGGGCGCGGTGGCTCATGCCTGTAATCC
-----+-----+-----+-----+-----+-----+-----+

3910          3930          3950
      .      .      .      .      .      .
CAGCGCTTTGAGAGGCCGAGGCGGGTGGATCACGAGATCAGGAGATTGAGACCATCCTGG
-----+-----+-----+-----+-----+-----+-----+

3970          3990          4010
```

FIG. 29



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```
CCAAAATGGTGAAACCTCGTCTCTGCTAAAAATACAAAAGTTAGCTGGGGGTGGTAGCGC
-----+-----+-----+-----+-----+-----+-----+
4030          4050          4070
GCGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCAGGGAGT
-----+-----+-----+-----+-----+-----+-----+
4090          4110          4130
CGGAGGTTGCAGTGAGCCAAGATCGCGCCGCTGCACTCCAGCCTGGCGACAGAGGGAGAC
-----+-----+-----+-----+-----+-----+-----+
4150          4170          4190
TCCATCTCAAAAAAAAAAAAAAAAAAAGTTAACATCTCATCCAAATTTGCACCGAGTA
-----+-----+-----+-----+-----+-----+-----+
4210          4230          4250
GGAAAACAAAAGTTTAAACATGAAACAGATGTTACTGAGGCCGAAAGGGTCTCCCAGGC
-----+-----+-----+-----+-----+-----+-----+
4270          4290          4310
CTGGGAGTCTGCAGCTTTTATGCAATTCTGCCCTCTGGCCACCGCCAGGGAAGAAAGTT
-----+-----+-----+-----+-----+-----+-----+
4330          4350          4370
GTCTCCGTCTGCTGCATCGCCTTTGCCAGCAATGAAGCCCCCAAGACAGCGGCAGCCGG
-----+-----+-----+-----+-----+-----+-----+
4390          4410          4430
TTGCCTGAACCTTCCTATCCTTGGGGGCACCCAGTGCAGGTGGATGACCCGACTCAACCT
-----+-----+-----+-----+-----+-----+-----+
4450          4470          4490
CCGCCAGGGCACCCCTCGGGGCAGGACGGGTAGCAAGGAGGGACAGAGATCGGCCCCAGG
-----+-----+-----+-----+-----+-----+-----+
4510          4530          4550
AGACCACGGAAGATCGCGCTCCTGGGGCCAACTTCAGCAGCGAGAGGCGGCCTTTGCCCA
-----+-----+-----+-----+-----+-----+-----+
```

FIG. 29



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AGGCGCGGTGGTGGTGGCGGGGATGGGTTCTGCTCAGAGCTCGGGTCAGCGCGGGAGGG  
-----+-----+-----+-----+-----+-----+-----+  
5170 5190 5210  
TCTCACGGCCCCGGCACCATACGGCCAGTAGGTCAGGGCGTGGGGACTCTTTGGGGGGGT  
-----+-----+-----+-----+-----+-----+-----+  
5230 5250 5270  
CTCCGTGGGACCTGCCCAGGGACGCTCAAGTGTGCTTGGGCTGGCCCCGGGCCCGGACTT  
-----+-----+-----+-----+-----+-----+-----+  
5290 5310 5330  
GCCCACACTGCCCGGCTGCCACTCCGCTGGCAAAGCAGAGGGCATGGCTCCCTCCCCCTC  
-----+-----+-----+-----+-----+-----+-----+  
5350 5370 5390  
GGGGACAGCCCAGCCCCAGCCCCAGCCCCATAGCCGTAGCCCCCTCTGCCTGGATTCTC  
-----+-----+-----+-----+-----+-----+-----+  
5410 5430 5450  
GCTCTCACAACCAGCTTCCATCCGCAGGCCACCGTGTGACCCGCTCCTGCTCCTCCACCC  
-----+-----+-----+-----+-----+-----+-----+  
5470 5490 5510  
CTTAGGACTCAGCGGGGCTCCATCCTCTAGGAAGCCCCCATGCCAAGAGTCCCCCAGAG  
-----+-----+-----+-----+-----+-----+-----+  
5530 5550 5570  
TCCCTGCTTTGCTCTCAGGCTGCAGAACTAGCTGTGGCCTCCACCCTGCTCACCCCTCGT  
-----+-----+-----+-----+-----+-----+-----+  
5590 5610 5630  
CCCTCCTCCCAGGGCAGCAGGGCAGTGTGTATGTTGTTTATATTGTTGCCTTGTGTTGGTG  
-----+-----+-----+-----+-----+-----+-----+  
5650 5670 5690  
AGATAGAGAAGGGCCTCTCCAGATAGAAGGTGTCTGTTTAGCAGTGCTCTGGAAAGACTG  
-----+-----+-----+-----+-----+-----+-----+

FIG. 29

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```
5710          5730          5750
CAGCTGTCTCCTCGGGGTAACCCCTCCAAACAAAGATGTTAAGATGGGGCTGGAACAACC
-----+-----+-----+-----+-----+-----+-----+

5770          5790          5810
TCTGCAAGCGGGTGGGAGGATTAGCCAGTCCTGCACAGCAAGTGCCTGGCCGGGAACAGG
-----+-----+-----+-----+-----+-----+-----+

5830          5850          5870
GAGGGCAACCAGGGAGGGGGGCATGCGGGGCTGGGCTGTGCTATGCAGACTGGGCGGTGGC
-----+-----+-----+-----+-----+-----+-----+

5890          5910          5930
TTCCACAGCACTGTGTGGGGACCAACAGGTACAGGGGCCTGGTCTGTTCTGGCCCCAGG
-----+-----+-----+-----+-----+-----+-----+

5950          5970          5990
GGAGGGCCCCAGGCGGTCCACTGCTCCCTCCCCCTCTGAGCCCTATCCTGGGGTCAGGGGA
-----+-----+-----+-----+-----+-----+-----+

6010          6030          6050
GGTGATGGGACCCCTGGGAGAGGGGCGTCTATGTGCCCAATACCAGCCTGGCTCCCTCGG
-----+-----+-----+-----+-----+-----+-----+

6070          6090          6110
GTTCCACCCCATTCACCCGGTCACCGGAGCTCCAGCTCCAGCTCCAGCTCTGCCCCCTCT
-----+-----+-----+-----+-----+-----+-----+

6130          6150          6170
CTCCCTCATTGGGGTCAGGGTGCCCGTGGCCAGCACGTGCGCGCAAGGCCATGTGGACAG
-----+-----+-----+-----+-----+-----+-----+

6190          6210          6230
CACCCACACACCACACTGCACCCACACCACACCTGTGCCCGGGGCCACCCTACCTCTTCC
-----+-----+-----+-----+-----+-----+-----+

6250          6270          6290
```

FIG. 29

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```
CCAAACCCTTAGAGGCCTAGGAGCAGCAAAGCTTGGTTCTCTACTCTCAGTTAAGTGCTC
-----+-----+-----+-----+-----+-----+-----+
6310          6330          6350
TCTGGGCTGAGAGACCTCCCCTCCTTCCCCCTCCCCCACATCCACTCAGAGCCCTCCCTGC
-----+-----+-----+-----+-----+-----+-----+
6370          6390          6410
ACTGGCCCCTCTAGCCTCCTTTCCAAGGTGGCAGACTCCTCTCGGCCCTCATCTGCCTGA
-----+-----+-----+-----+-----+-----+-----+
6430          6450          6470
TGGCAATTCACTCATCCAATCAAGGAGGGCTTCTTGGAGGAAGGGTCTTTGATGTTTGTA
-----+-----+-----+-----+-----+-----+-----+
6490          6510          6530
GTCTGGGAGAGAAGGTGGAGGAGAAAAAAGGAGTTGGGGTGGCCTAGCAGGAGCTGAGTC
-----+-----+-----+-----+-----+-----+-----+
6550          6570          6590
ACTTCCACAGGCAGCCATCAGCCCAGCAGGACTGAGGCCAGGGCTGCGTGGAGGGGGGAG
-----+-----+-----+-----+-----+-----+-----+
6610          6630          6650
GCTGTCTGTTCTGGGAGCTGGGACTGGGTACCGGGGGAAGGAGGGCTGCTGCAGGCTCTG
-----+-----+-----+-----+-----+-----+-----+
6670          6690          6710
GGTGCCTGGGGCCTGGCTCCTGCAGGGCGGGCCTGTGAGAGTGGTTGGGGCCAGTGGAGG
-----+-----+-----+-----+-----+-----+-----+
6730          6750          6770
GGCTGGGAGCATTCCAGGGGAACATTCCAGGCGCCCTCTGAGTAATGCTTGGCTCTGGGA
-----+-----+-----+-----+-----+-----+-----+
6790          6810          6830
TTCCTCCTAGAGCCCCCTTAGGCACACCCGGCCAGGGAGCACCAAGGCTCCGTCCGGAAG
-----+-----+-----+-----+-----+-----+-----+
```

FIG. 29

Variable	Mean	SD	Min	Max	Skewness	Kurtosis	Normality
Age	35.2	12.5	18	65	0.15	3.2	0.98
Gender	1.2	0.4	1	2	0.05	2.8	0.99
Education	12.5	2.1	9	16	0.25	3.5	0.97
Income	1500	500	500	3000	0.35	3.8	0.96
Health	2.5	0.8	1	4	0.10	3.1	0.99
Stress	3.2	1.1	1	5	0.20	3.4	0.98
Quality of Life	4.5	1.2	2	7	0.18	3.3	0.98
Depression	1.8	0.9	1	4	0.12	3.2	0.99
Life Satisfaction	5.2	1.0	3	7	0.16	3.3	0.98
Resilience	3.8	1.1	2	6	0.14	3.2	0.99
Optimism	4.1	1.0	2	6	0.17	3.3	0.98
Self-Esteem	4.3	1.1	2	6	0.19	3.4	0.97
Life Purpose	4.6	1.2	2	7	0.21	3.5	0.96
Gratitude	4.8	1.0	2	7	0.13	3.2	0.99
Forgiveness	4.4	1.1	2	7	0.15	3.3	0.98
Compassion	4.7	1.0	2	7	0.16	3.3	0.98
Kindness	4.9	1.1	2	7	0.18	3.4	0.97
Generosity	4.6	1.2	2	7	0.20	3.5	0.96
Patience	4.5	1.1	2	7	0.17	3.3	0.98
Humility	4.3	1.0	2	7	0.19	3.4	0.97
Modesty	4.1	1.1	2	7	0.21	3.5	0.96
Shame Avoidance	3.9	1.0	2	7	0.14	3.2	0.99
Self-Compassion	4.2	1.1	2	7	0.16	3.3	0.98
Transcendental Meditation	4.4	1.2	2	7	0.18	3.4	0.97
Vipassana Meditation	4.6	1.1	2	7	0.17	3.3	0.98
Transcendental Meditation	4.8	1.0	2	7	0.15	3.2	0.99
Vipassana Meditation	4.7	1.1	2	7	0.16	3.3	0.98
Transcendental Meditation	4.5	1.2	2	7	0.19	3.4	0.97
Vipassana Meditation	4.3	1.0	2	7	0.21	3.5	0.96
Transcendental Meditation	4.1	1.1	2	7	0.14	3.2	0.99
Vipassana Meditation	3.9	1.0	2	7	0.16	3.3	0.98
Transcendental Meditation	4.2	1.1	2	7	0.17	3.3	0.98
Vipassana Meditation	4.0	1.2	2	7	0.18	3.4	0.97
Transcendental Meditation	4.3	1.0	2	7	0.20	3.5	0.96
Vipassana Meditation	4.1	1.1	2	7	0.15	3.2	0.99
Transcendental Meditation	3.9	1.0	2	7	0.16	3.3	0.98
Vipassana Meditation	4.2	1.1	2	7	0.17	3.3	0.98
Transcendental Meditation	4.0	1.2	2	7	0.18	3.4	0.97
Vipassana Meditation	4.3	1.0	2	7	0.20	3.5	0.96
Transcendental Meditation	4.1	1.1	2	7	0.15	3.2	0.99
Vipassana Meditation	3.9	1.0	2	7	0.16	3.3	0.98
Transcendental Meditation	4.2	1.1	2	7	0.17	3.3	0.98
Vipassana Meditation	4.0	1.2	2	7	0.18	3.4	0.97
Transcendental Meditation	4.3	1.0	2	7	0.20	3.5	0.96
Vipassana Meditation	4.1	1.1	2	7	0.15	3.2	0.99
Transcendental Meditation	3.9	1.0	2	7	0.16	3.3	0.98
Vipassana Meditation	4.2	1.1	2	7	0.17	3.3	0.98
Transcendental Meditation	4.0	1.2	2	7	0.18	3.4	0.97
Vipassana Meditation	4.3	1.0	2	7	0.20	3.5	0.96
Transcendental Meditation	4.1	1.1	2	7	0.15	3.2	0.99
Vipassana Meditation	3.9	1.0	2	7	0.16	3.3	0.98
Transcendental Meditation	4.2	1.1	2	7	0		

FIG. 29

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CACCCTGTGCTCTGTCTTTACTCCAGGACATATCCCTGGGCAGCCAGTCACCCCGCACTG  
-----+-----+-----+-----+-----+-----+-----+

7450

7470

7490

GGTCCTGGATGGACAACCCTGGCGCACCGTCAGCCTGGAGGAGCCGGTCAGTGCCATGTC  
-----+-----+-----+-----+-----+-----+-----+

7510

7530

7550

TCCCCGCCCTCCACAGGGGCCCTGAACCTCCCAGCCCTTTTGTCTCTCCCTACATTACAG  
-----+-----+-----+-----+-----+-----+-----+

7570

7590

7610

CTTCTAGTTTTTGTGGGGTCCCCAGAACCACCAAGTCACTACTCTATAGGCCCTGCCT  
-----+-----+-----+-----+-----+-----+-----+

7630

7650

7670

CCCCTGCCCTCAAGTGGGCAGAAGAAGGCACTGGGGTTTGGACATCTGGATCTCGTGAG  
-----+-----+-----+-----+-----+-----+-----+

7690

7710

7730

CCCGCACACATGGAAGTCATTTTCAGCTTTCTCCACCCCACTCCCTCTTTCCCTCCCTCC  
-----+-----+-----+-----+-----+-----+-----+

7750

7770

7790

CTGGATGATCTGGGCCACCCCCACCCCCACCAGGCAGAAATGGGTCCAGAGTTTGTGGGT  
-----+-----+-----+-----+-----+-----+-----+

7810

7830

7850

CCTGAAGCTTTTCAGGAGCCTCTAAAAAAAAAAAAAAAAAAAAAGCACCAAAAAGAAAA  
-----+-----+-----+-----+-----+-----+-----+

7870

7890

7910

CCTTTTGCAAAGTTGACCAGAACATGTGACCCTGTGGACACACTGCTGTCCCTCTCAGGG  
-----+-----+-----+-----+-----+-----+-----+

7930

7950

7970

CCCTGCCACGAAGGCCTGAACCTTCAGCCTCACTGGCTCCTGTGGAATCCACTTCTGGTA  
-----+-----+-----+-----+-----+-----+-----+

FIG. 29

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```
7990      8010      8030
TGGGGGGGGCAGTGGTCACTCTCCTGATGTCCCCCAGATGTAAGACCACCCCATGTGCTT
-----+-----+-----+-----+-----+-----+-----+

8050      8070      8090
CTTCTGCAGGACGCTCTGCCCCAGCCTCTTCCCAATCCCGCTCTTCACACGCTTCCAGAA
-----+-----+-----+-----+-----+-----+-----+

8110      8130      8150
TAACCATGCCCCATCTGTTTGTGCCATAATATCTGTGCTGCAAACTAAGAGGGCAGTAGC
-----+-----+-----+-----+-----+-----+-----+

8170      8190      8210
CTTGATATGCTCATTTTACAGAGGGGCAAACGGAAGCCCAGAGAGCTTGGGGAAATTGTC
-----+-----+-----+-----+-----+-----+-----+

8230      8250      8270
CATGGTCACACAGCTCTTTAGGCTGGGAGCCTGAGACCCACTAAGGTCTGAACGATTTTA
-----+-----+-----+-----+-----+-----+-----+

8290      8310      8330
AACCATTGGCTACACCCCTGCCCCTCCTAGAGAGCCCTCTTTGTTTGAATTTTCAGCCC
-----+-----+-----+-----+-----+-----+-----+

8350      8370      8390
TACTGTCCAAATCCAGCAAGAGGGAAGGCAGGGGAGCATTGCCATGAAGGCTGAGAGGCC
-----+-----+-----+-----+-----+-----+-----+

8410      8430      8450
CCCAGAGACCCAGCAGCTCCCAACCCAGGGCCCTCACTGGGATCCCCTAGGCCCATAAGG
-----+-----+-----+-----+-----+-----+-----+

8470      8490      8510
CCCCCATTCCTACTGGTCAAGCACGGCACTGGCCTGAGCTTTGAGATTGCCCTCCCCATCC
-----+-----+-----+-----+-----+-----+-----+

8530      8550      8570
```

FIG. 29



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CCAGGAGGGGAAGGCTGGACACACACTGGGGTCACTCTGCCTCTGGGCCTCCCTGTCTGT  
-----+-----+-----+-----+-----+-----+-----+  
8590 8610 8630  
CTGGCCTGGGCTGTGACCAAGAGGAGAGCCCCAAAGGGGCTCTGCTTCCCCACCGGTGG  
-----+-----+-----+-----+-----+-----+-----+  
8650 8670 8690  
GCCCCTGCCCCCAGGAAGCCTGCCAAGATGGTACAGAAGAAAGAGTAGAGGCTAGGTATC  
-----+-----+-----+-----+-----+-----+-----+  
8710 8730 8750  
CCCTCCAAAAGGCAGGAAACACTCACATTTCAAGATGAGGGGTATATATCAAGGGGCAGG  
-----+-----+-----+-----+-----+-----+-----+  
8770 8790 8810  
GTACCAGGAGGGCAAGAGTAAAGATAGCAGGGGCTGCAGAGGAACAGGGACCTCGAGTAT  
-----+-----+-----+-----+-----+-----+-----+  
8830 8850 8870  
GGCCTTTTTCCCGGTGCAGACCTTTCCCCAATAAAGCAAGTGGCATTCCAGCCTCATGAG  
-----+-----+-----+-----+-----+-----+-----+  
8890 8910 8930  
CTCATGCTGGAGGCCTTGTGGGGCCTGTGGCCAGGGAGGCAAGGACCATCTGCTCCCCAC  
-----+-----+-----+-----+-----+-----+-----+  
8950 8970 8990  
TTGCGAAGGAAGAACTCCCTCCAAAGACTCTGAGACCCTTGGACAGGGCCCCAGGCCAGT  
-----+-----+-----+-----+-----+-----+-----+  
9010 9030 9050  
GCATTTTTTGAGAAAAGGAGTCGGGGGTAAACATTCCGAAGGCGCAGCAGCCTCCCAGG  
-----+-----+-----+-----+-----+-----+-----+  
9070 9090 9110  
AAGCTCCTGGGCCGGCTCCAACCTCTGGGCCCCAGCCAGGCTGAGTGGACAAGGGGGAAG  
-----+-----+-----+-----+-----+-----+-----+

FIG. 29

[illegible]

FIG. 29

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CATCTTTGTATGTTCTCACCTCCTCCACGCCCTCCATAGTATGTGGGGGGTCCTGCTGAC  
-----+-----+-----+-----+-----+-----+-----+  
9730 9750 9770  
TCCCCAGCCACGTTCTCCCCAAGAACTTCCTCCCCAGCCGGCTCCACAGGCCACCTACT  
-----+-----+-----+-----+-----+-----+-----+  
9790 9810 9830  
CCCTGGCAGGCAGGAGGCCTGGAGGCCACCATCTCAGCTCCACACTCTTTTCTTGCCCAGG  
-----+-----+-----+-----+-----+-----+-----+  
9850 9870 9890  
TCTCGAAGCCAGACATGGGGCTGGTGGCCCTGGAGGCTGAAGGCCAGGAGCTCCTGCTTG  
-----+-----+-----+-----+-----+-----+-----+  
9910 9930 9950  
AGCTGGAGAAGAACCAGTGAGTGCCAGGCTGGGGTAGGGCTGGGAGGAGGGGATCAGTGT  
-----+-----+-----+-----+-----+-----+-----+  
9970 9990 10010  
TGGGGGGCAGGGACTGACACAGATCTGTGCGGGTGGCTGGATGGGCAGAGGACCCCAGAG  
-----+-----+-----+-----+-----+-----+-----+  
10030 10050 10070  
AGGGTGCAGATGACAGGGAGAGTCACGCAGGCCTGTGGTTGGCTCCCTGGAGGCTGAAGA  
-----+-----+-----+-----+-----+-----+-----+  
10090 10110 10130  
GGACCGCTGAGGCTGTCAGCCCCGCTGTGGGGCACCTCCGCCCTCCCAACCCCAGGAGCG  
-----+-----+-----+-----+-----+-----+-----+  
10150 10170 10190  
GCTTGTTAGCTCCCTGCTGGCGATGAGTGAGCACCTAGTGGACATTTGCAAGATATG  
-----+-----+-----+-----+-----+-----+-----+  
10210 10230 10250  
CTGAGTCTAAAGAAATCCTAGAGGGAAAAGATGAGCCGGCACCCCAGGCTAAGGGAATGG  
-----+-----+-----+-----+-----+-----+-----+

FIG. 29

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```
10270      10290      10310
CAGGGACCAAGATGCGGTGGCTTTGGGAGGCCGAGGCGGGCGGCTCACCTGAGGTCAGGA
-----+-----+-----+-----+-----+-----+-----+

10330      10350      10370
GTTTGAGACCAGCCTTGCCAACATGGTGAAACCCCGTCTCTACTAAAAATACAAAAAATT
-----+-----+-----+-----+-----+-----+-----+

10390      10410      10430
AGCCAGGCGTGGTGGCGGCGCCTGTAATCCCAGCTACTTAGGGGGCTGAGACGGGAGAAT
-----+-----+-----+-----+-----+-----+-----+

10450      10470      10490
CGCTTGAACCCCGAGGTAGAGGTTGTGGTGAGCCAAGATCACACCACTGCACCACTCCG
-----+-----+-----+-----+-----+-----+-----+

10510      10530      10550
GCCTGGGCAAAGAGTGAGACTCCGTCTCAAAAAAAGAGAAAAAAGAAAAAGAAAAAA
-----+-----+-----+-----+-----+-----+-----+

10570      10590      10610
AAAAGAAAGAAAGAAAAAGAAAAAGATGCAGTGGCTACACTTGGGGGCAGCAGTTTGT
-----+-----+-----+-----+-----+-----+-----+

10630      10650      10670
CTGACCTGCCTGGAAGGTCTCCATCTACAGGGAGGGGAGCAGGGGGGAATGAATTTGGAG
-----+-----+-----+-----+-----+-----+-----+

10690      10710      10730
AGTCCCAGGAGGGCCAGATCACAGAAGGCCATTTTGGTGCTCAGTGTCTTGGACCATCCA
-----+-----+-----+-----+-----+-----+-----+

10750      10770      10790
GAGCCAAAGATTTTGAGCTGGGGAAGGGACAGGCAGACCTGTGCTCAGGAAGGTGCCTTG
-----+-----+-----+-----+-----+-----+-----+

10810      10830      10850
```

FIG. 29

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```
GGCTGGGTGGGTGGGTGTCCGGGCTGGAGCGCAGGCTCTTAAACCACCCAGATTATGT
-----+-----+-----+-----+-----+-----+-----+
10870              10890              10910
TATCAGTATATATCACCTACTGAGTGCTTGACCGCAGGCGCTGTTCTGAGCACTTGACAC
-----+-----+-----+-----+-----+-----+-----+
10930              10950              10970
GTATTTTATTCTCCCTCGTGGAGTCGGATGGACAGGGAACAACTCTAGTTCCACTGTGC
-----+-----+-----+-----+-----+-----+-----+
10990              11010              11030
CCAACCATATTTTCCCGACGTCCCTACCCTTTCAATGGGGTGGTCACATCACCTACCTCC
-----+-----+-----+-----+-----+-----+-----+
11050              11070              11090
TAGGGTGGCGGGTGTGTGTGGGGCAGGGGTAGGGGGCAGAGCTGGGGCAGGTGGTGGAAT
-----+-----+-----+-----+-----+-----+-----+
11110              11130              11150
GCCTGGGAGGGGGGAAGCAGCCATCATTAGCGGGTGGTCTGGAGGTAATGAGGCCAAGGT
-----+-----+-----+-----+-----+-----+-----+
11170              11190              11210
GAGGTTGGGTAAAGGATTTTCTTTAAAGAAGACAGATTGACTTATGATTGATCCATCCGT
-----+-----+-----+-----+-----+-----+-----+
11230              11250              11270
GTGGGAAAGATCCTGTTGAGATGGAGCCTGAAGATGGAATCATTACCGGAGTGGGTGTGG
-----+-----+-----+-----+-----+-----+-----+
11290              11310              11330
AGAAGGCAGGGAGGGTGAAGCAGCGTGGGCAGGTGGCGATTCTGTTTTCTCTGGAGGCA
-----+-----+-----+-----+-----+-----+-----+
11350              11370              11390
GGGGGTGAGCATCAATCACTGAAGGACAGGTGGGAGGTATGTGGGGTCTAGAAGTCTGAG
-----+-----+-----+-----+-----+-----+-----+
```

FIG. 29



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GGCCCCCAACCACACGGTGAGATGCTTCCATGGGCTCTGGGATGCACCGCCAGAGGTACC  
-----+-----+-----+-----+-----+-----+-----+

12010 12030 12050  
CCCCCACCATTCCCTACCCCTACTCCTCCTTGCATTCTTAAGGGGCGGTTGGAGCCAGCCC  
-----+-----+-----+-----+-----+-----+-----+

12070 12090 12110  
CTACCACACCCTCCCTCTTGCCCTCTTGCTCCAGCCCTGGCTGAGATTGGGGCTGGCC  
-----+-----+-----+-----+-----+-----+-----+

12130 12150 12170  
CCTTCCTCCCTAGGATCATTTGCCACTACCAAGGGCGAGTAAGGGGCTTCCCCGACTCCTG  
-----+-----+-----+-----+-----+-----+-----+

12190 12210 12230  
GGTAGTCCTCTGCACCTGCTCTGGGATGAGGTGAGCTCTGGGAGAGGAGGCTGGGCCTGG  
-----+-----+-----+-----+-----+-----+-----+

12250 12270 12290  
GATGGGGAAAGAGCTCCCTCACACCCGCTCCTACCCCTCTGCACCCTAGTGGCCTGATCA  
-----+-----+-----+-----+-----+-----+-----+

12310 12330 12350  
CCCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGACT  
-----+-----+-----+-----+-----+-----+-----+

12370 12390 12410  
TCTCAACCCACGAGATCTTTTCGGATGGAGCAGCTGCTCACCTGGAAAGGAACCTGTGGCC  
-----+-----+-----+-----+-----+-----+-----+

12430 12450 12470  
ACAGGGATCCTGGGAACAAAGCGGGCATGACCAGCCTTCCTGGTGGTCCCCAGAGCAGGG  
-----+-----+-----+-----+-----+-----+-----+

12490 12510 12530  
TCAGGGGCATCGATCGGATGGGAGTGGGAATGCTGTATCTATAGCCCTCCAAATCAGAAG  
-----+-----+-----+-----+-----+-----+-----+

FIG. 29

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```
12550      12570      12590
AGACAGGAATTACAGGCCTCGAGTCCCAGTATTTTATTGAAGTCTGAAGAAACAAGTT
-----+-----+-----+-----+-----+-----+-----+

12610      12630      12650
CCAGAAAACATGTTAAACTTCCTTCTGGGAGCTGGGGTTGGGGGTCAGGGCTCAAGCCCA
-----+-----+-----+-----+-----+-----+-----+

12670      12690      12710
GCAGCTTCCACTCAGGGTCCCCATTTGCACCTCCGCAGGGCAGGCGAGAAGCGCGCAGGA
-----+-----+-----+-----+-----+-----+-----+

12730      12750      12770
CCCGGAAGTACCTGGAACGTACATTGTGGCAGACCACACCCTGGTGAGGAGAGACCCCA
-----+-----+-----+-----+-----+-----+-----+

12790      12810      12830
GGGGTTGGCGGGGTCAGGGATGGGGCCAGCTCAGCCCCTCAAGCCACCGGGATTTCTGCC
-----+-----+-----+-----+-----+-----+-----+

12850      12870      12890
TTCCCAGTTCTTGA CTGCGCACCGAAACTTGAACCACACCAAACAGCGTCTCCTGGAAGT
-----+-----+-----+-----+-----+-----+-----+

12910      12930      12950
CGCCAACTACGTGGACCAGGTTGGGGGCGGCGGGGAGAGAGCGGTGATGGGGGTGGCGGC
-----+-----+-----+-----+-----+-----+-----+

12970      12990      13010
GGCAGGACAGGCAGGTGCTGGTGGGGTTTGGGGAAGAGGAAGGGCGCCCCACGAAGGACC
-----+-----+-----+-----+-----+-----+-----+

13030      13050      13070
ACCGGCGCGATGGGGCGCCCTGTCCCGGCTTCAGCCCCGCCTCGCCCTCAGCTTCTCAGG
-----+-----+-----+-----+-----+-----+-----+

13090      13110      13130
```

FIG. 29



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ACTCTGGACATTTCAGGTGGCGCTGACCGGCCTGGAGGTGTGGACCGAGCGGGACCGCAGC  
-----+-----+-----+-----+-----+-----+-----+

13150 13170 13190  
CGCGTCACGCAGGACGCCAACGCCACGCTCTGGGCCTTCCTGCAGTGGCGCCGGGGGCTG  
-----+-----+-----+-----+-----+-----+-----+

13210 13230 13250  
TGGGCGCAGCGGCCCCACGACTCCGCGCAGCTGCTCACGTGGGTGCCCTCTGACCCGGACG  
-----+-----+-----+-----+-----+-----+-----+

13270 13290 13310  
CGGGTCCCGGTGGGGCGGCCTCACCTCCCGGCCCCGCCTGGTCACGCCGCGCTCCGCCC  
-----+-----+-----+-----+-----+-----+-----+

13330 13350 13370  
CCAGGGGCCGCGCCTTCCAGGGCGCCACAGTGGGCCTGGCGCCCGTCGAGGGCATGTGCC  
-----+-----+-----+-----+-----+-----+-----+

13390 13410 13430  
GCGCCGAGAGCTCGGGAGGCGTGAGCACGGTGAGCCCCGCGGGCGGGGGCGAGGGAGAGA  
-----+-----+-----+-----+-----+-----+-----+

13450 13470 13490  
CAGGAGGCTCTACGGCCGAGTGACCGCCCTCCACGGCCCCCAGGACCACTCGGAGCT  
-----+-----+-----+-----+-----+-----+-----+

13510 13530 13550  
CCCCATCGGCGCCGAGCCACCATGGCCCATGAGATCGGCCACAGCCTCGGCCTCAGCCA  
-----+-----+-----+-----+-----+-----+-----+

13570 13590 13610  
CGACCCCGACGGCTGCTGCGTGGAGGCTGCGGCCGAGTCCGGAGGCTGCGTCATGGCTGC  
-----+-----+-----+-----+-----+-----+-----+

13630 13650 13670  
GGCCACCGGGTACGCGGGTGGGGGGTGGGGGCTGCGGCGGGGCGGCTAGTCCTGGGGACT  
-----+-----+-----+-----+-----+-----+-----+

FIG. 29

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13690	13710	13730
TCCTCCGCTGCGTTTCTTTGGTCGTCCTCAGTTTCCTCTTCTGTAAAATGGGGATAATG		
-----+-----+-----+-----+-----+-----+-----+		
13750	13770	13790
ATCATAGTGTCCGCTTCAGGGTGGTTTATGAGGCTTAAAGGGAAGAAGCTCAGGCAAAGT		
-----+-----+-----+-----+-----+-----+-----+		
13810	13830	13850
GGATTCTCAACGGTATGAAGATTATTTTCCGAGTAACCTGGCGAGGTTACTCCTACACCG		
-----+-----+-----+-----+-----+-----+-----+		
13870	13890	13910
GGAGGAGCACCGTCGGGTCGCGATTCCACCTTGGGTCCCGGGCTGCTCACTATTGGGGCC		
-----+-----+-----+-----+-----+-----+-----+		
13930	13950	13970
GCATCGTCCCCTGTCCCGCTTGTGTGTGACTTTGCGCGGGTTACTTCCCCTCTCTGGGC		
-----+-----+-----+-----+-----+-----+-----+		
13990	14010	14030
TCTGCGCGTCTGGCGGCTGTAGCCAAGCCCAGGGGTGGGGATCAGAGAAGCGCGGGGGTT		
-----+-----+-----+-----+-----+-----+-----+		
14050	14070	14090
GGGGGACTGTCCCTCCATGCCCAATGCCCTCCCCGTGCCGGTAGGCACCCGTTTCCGCGC		
-----+-----+-----+-----+-----+-----+-----+		
14110	14130	14150
GTGTTTCAGCGCCTGCAGCCGCCGCGCTGCGCGCTTCTTCCGCAAGGGGGCGGCGCT		
-----+-----+-----+-----+-----+-----+-----+		
14170	14190	14210
TGCCTCTCCAATGCCCCGACCCCGACTCCCGGTGCCGCCGGCGCTCTGCGGGAACGGC		
-----+-----+-----+-----+-----+-----+-----+		
14230	14250	14270

FIG. 29

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```
TTCGTGGAAGCGGGCGAGGAGTGTGACTGCGGCCCTGGCCAGGTTAAGTCGGCTCGCCCCG
-----+-----+-----+-----+-----+-----+-----+
14290              14310              14330
GCCCCCACTTGCCCTCTCCGCTCAGGTCTGGGGCGCTGCGCCCTCACCTGGGCCCCTTCTT
-----+-----+-----+-----+-----+-----+-----+
14350              14370              14390
GCCTTTCTGGTCCCAGGAGTGCCGCGACCTCTGCTGCTTTGCTCACAACTGCTCGCTGCG
-----+-----+-----+-----+-----+-----+-----+
14410              14430              14450
CCCCGGGGGCCAGTGCGCCACGGGGACTGCTGCGTGCGCTGCCTGGTGAGGGCATGGAA
-----+-----+-----+-----+-----+-----+-----+
14470              14490              14510
GGTTCAGGGTGAGGGTTTCGGGGAGCTTGGGAGCCGGCCTGTTGGCCTTAGTTAATTGGT
-----+-----+-----+-----+-----+-----+-----+
14530              14550              14570
GCCCTCAGGTTCCCCCGTTGGGTGCTGGGCTTGGGTAGGCCTGGCTCCCCCAGCTCCGAG
-----+-----+-----+-----+-----+-----+-----+
14590              14610              14630
CCGCGCTCTCGGCATGGACCTCTCACTGCACGTGGCCTCTCTCTGCCTTCCCCACCAACC
-----+-----+-----+-----+-----+-----+-----+
14650              14670              14690
GTCACCTGCGCAGCTGAAGCCGGCTGGAGCGCTGTGCCGCCAGGCCATGGGTGACTGTGA
-----+-----+-----+-----+-----+-----+-----+
14710              14730              14750
CCTCCCTGAGTTTTGCACGGGCACCTCCTCCCACTGTCCCCCAGACGTTTACCTACTGGA
-----+-----+-----+-----+-----+-----+-----+
14770              14790              14810
CGGCTCACCTGTGCCAGGGGCAGTGGCTACTGCTGGGATGGCGCATGTCCCACGCTGGA
-----+-----+-----+-----+-----+-----+-----+
```

FIG. 29

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14830 14850 14870  
GCAGCAGTGCCAGCAGCTCTGGGGGCTGGTGAGAGGACACGAGCACCCCTTGCACCCTGC  
-----+-----+-----+-----+-----+-----+-----+  
14890 14910 14930  
CCCCCATCCTCTGGTGGGGCCAGTTTCTACTGTGGGGAAGATGGGCAGGGGAACTGAG  
-----+-----+-----+-----+-----+-----+-----+  
14950 14970 14990  
GCCCCGTGAGCGCAGCCCCCTCTCCGAGCTGCCCCAGCCTGGCCCATGCTTCCTCAGGCT  
-----+-----+-----+-----+-----+-----+-----+  
15010 15030 15050  
CCCCCCCAGCTCCCGAGGCCTGTTTCCAGGTGGTGAACCTCTGCGGGAGATGCTCATGGAA  
-----+-----+-----+-----+-----+-----+-----+  
15070 15090 15110  
ACTGCGGCCAGGACAGCGAGGGCCACTTCCTGCCCTGTGCAGGGAGGTAGGGAGTGGAGC  
-----+-----+-----+-----+-----+-----+-----+  
15130 15150 15170  
TGAGTGGAGGGAGCAGAAGCTATGGAGTGGGTTTGGGGAAGGGGGGTACTGCAGCTGTTG  
-----+-----+-----+-----+-----+-----+-----+  
15190 15210 15230  
ACCCCCCTCTACTTCCTCCCCAGGGATGCCCTGTGTGGGAAGCTGCAGTGCCAGGGTGGGA  
-----+-----+-----+-----+-----+-----+-----+  
15250 15270 15290  
AAGCCCAGCCTGCTCGCACCGCACATGGTGCCAGTGGACTCTACCGTTCACCTAGATGGC  
-----+-----+-----+-----+-----+-----+-----+  
15310 15330 15350  
CAGGAAGTGACTTGTCGGGGAGCCTTGGCACTCCCCAGTGCCAGCTGGACCTGCTTGGC  
-----+-----+-----+-----+-----+-----+-----+  
15370 15390 15410

FIG. 29

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CTGGGCCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAATGGTGAGCTCTGCCCACCCG  
-----+-----+-----+-----+-----+-----+-----+  
15430 15450 15470  
ACCCCTCCTTGCCGTTTGAATCCCGCAGGCCAGTGTCCCCCTCACTGCCTGGTGCATGC  
-----+-----+-----+-----+-----+-----+-----+  
15490 15510 15530  
CCGTAGGTGTGCCAGAGCAGGCGCTGCAGGAAGAATGCCTTCCAGGAGCTTCAGCGCTGC  
-----+-----+-----+-----+-----+-----+-----+  
15550 15570 15590  
CTGACTGCCTGCCACAGCCACGGGGTGAGAGCCCGAGGAGTGGGGGTGACCTTGGGGTTC  
-----+-----+-----+-----+-----+-----+-----+  
15610 15630 15650  
CTAATCCTACGTGACCCTCCTCTTCTCTCTCTGCAGGTTTGCAATAGCAACCATAACTG  
-----+-----+-----+-----+-----+-----+-----+  
15670 15690 15710  
CCACTGTGCTCCAGGCTGGGCTCCACCCTTCTGTGACAAGCCAGGCTTTGGTGGCAGCAT  
-----+-----+-----+-----+-----+-----+-----+  
15730 15750 15770  
GGACAGTGGCCCTGTGCAGGCTGAAAGTATGCCAGTGGGGGGCATGTGGGCAGGAGCTGG  
-----+-----+-----+-----+-----+-----+-----+  
15790 15810 15830  
GGTGGTGCACCTGCTCAGGACTCAGCGCCCCTTCCCCCAATCCCCGCAGACCATGACACC  
-----+-----+-----+-----+-----+-----+-----+  
15850 15870 15890  
TTCCTGCTGGCCATGCTCCTCAGCGTCCTGCTGCCTCTGCTCCCAGGGGGCCGCCTGGCC  
-----+-----+-----+-----+-----+-----+-----+  
15910 15930 15950  
TGGTGTGCTACCGACTCCAGGAGCCCATCTGCAGCGATGCAGCTGGGGCTGCAGAAGG  
-----+-----+-----+-----+-----+-----+-----+

FIG. 29

[illegible][illegible][illegible]

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ACCCAGTTCTCTGTGACCTGGGTGGTGGCGGAGTGGGGAGTCACATAATACTAAGCATGG  
-----+-----+-----+-----+-----+-----+-----+  
16570 16590 16610  
CTGTCCTAGGACTCACCTGACACAGGGCCCTAGGCAGGGCAGGCACCTCTGTGGCCATGT  
-----+-----+-----+-----+-----+-----+-----+  
16630 16650 16670  
CTGACATAGCCTGGTCTTGGGAGTGCTCCGGGCAAGCCAAGGGAGATGGCATGATTTGGG  
-----+-----+-----+-----+-----+-----+-----+  
16690 16710 16730  
CCAGAGATGGGGGCAGAGGGCATAACAGACAGGGGCAGGGCACCACCTGGGCCCCGGGTG  
-----+-----+-----+-----+-----+-----+-----+  
16750 16770 16790  
GCAGCTAAGAGGACCCTGACAAAGCGAGTTGTGATTGAGGGTCTGTGGGCAGAGGAGCAA  
-----+-----+-----+-----+-----+-----+-----+  
16810 16830 16850  
GGTGGCCAGAGCCTGGCGTGTGACACGGAGGGGGCGCTGCAGAGGGTGGCGGCTGCTTC  
-----+-----+-----+-----+-----+-----+-----+  
16870 16890 16910  
TCATCCCCAGGCGGGAGTCTCAGGGCAGGGGAGAATGTTTTGAAGGAACATCACAGGAAA  
-----+-----+-----+-----+-----+-----+-----+  
16930 16950 16970  
TGACAAGGCCTTGGGGGATGGGATGGGGACAGTCAAAGATGGCTTGAATCATCAAGGGC  
-----+-----+-----+-----+-----+-----+-----+  
16990 17010 17030  
AGCAGGGCAGCCAGGGGCAAGGAGAGCAGACATAGCTGCCGAAGGGGCGGACATCCAAGG  
-----+-----+-----+-----+-----+-----+-----+  
17050 17070 17090  
TTCTTTGGAAGCTGAGCGATGCCAGCATCTGGAGAGTGCCAGGCTGCTGGGTGGTGTGAG  
-----+-----+-----+-----+-----+-----+-----+

FIG. 29

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```
17110      17130      17150
AGCCTGGAGGAAATGTTAGGACTAGAGAGAGGAGGTGCCAGCCGAGGGCATGAGGCTCAC
-----+-----+-----+-----+-----+-----+-----+

17170      17190      17210
TTGGAGCCTGGATCCCAAGGCTCCCCTGAAGAGGGAGCAGGAAGGGAGCTGAGAGGGTGA
-----+-----+-----+-----+-----+-----+-----+

17230      17250      17270
CTTGGAGCAGATGGGTGCCCCAAGAACTCAGTAAACGCAGAACTCCCTGGGCTGGACAC
-----+-----+-----+-----+-----+-----+-----+

17290      17310      17330
CATGCTGCGGGGAGGCAATAACCCACTCAGGATCACTGTGCCAACCTCCTGGACTCTTAT
-----+-----+-----+-----+-----+-----+-----+

17350      17370      17390
CACGTTGCTCAGCCCCAAAGATGGCCCAACAGGGACCACCCCTGGGCGGCGTTTACCC
-----+-----+-----+-----+-----+-----+-----+

17410      17430      17450
CATGGAGTTGGGCCCCACAGCCACTGGACAGCCCTGGCCCCTGGGTGAGTGAGGCACCAG
-----+-----+-----+-----+-----+-----+-----+

17470      17490      17510
GGGGAGGTGGAGAGGGAAGGGAGAAGGGAAGGGCTCATGCCTCCTGCCTCCTTCCAGATG
-----+-----+-----+-----+-----+-----+-----+

17530      17550      17570
GGCAGCACCCAGTCACCTTGAGTCCCCTATGCCCTCCCCAGCCCCAGGGTCTCCTGCTG
-----+-----+-----+-----+-----+-----+-----+

17590      17610      17630
ACCATATTACAAACATTTACCCTCCACCATTTCTCCCAGACCCTGAGAACTCTCATGAGC
-----+-----+-----+-----+-----+-----+-----+

17650      17670      17690
```

FIG. 29



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CCAGCAGCCACCCTGAGAAGCCTCTGCCAGCAGTCTCGCCTGACCCCCAAGGTAGGCAGG  
-----+-----+-----+-----+-----+-----+-----+  
17710 17730 17750  
GACCTGGATTCAAAGCCTCCCCCTCTCATCGCCACCCCTCCACCTCTCCCACCCCTCAG  
-----+-----+-----+-----+-----+-----+-----+  
17770 17790 17810  
TTTGCTGCCCCCTAATCAGGTTTCTGGGCTCAGGTTATTATGGAAATGAGTTTATGACCT  
-----+-----+-----+-----+-----+-----+-----+  
17830 17850 17870  
CTTGCTTATCATGGAGACCAGGATGCTGGAAGCCCTGGGCTGGGGAGGGAGAAGCTGTG  
-----+-----+-----+-----+-----+-----+-----+  
17890 17910 17930  
GCTTTTCTGGATCACTGGTCTCACTGAGTGAGGATGGGCTCTCTGCCACACAGCTTGC  
-----+-----+-----+-----+-----+-----+-----+  
17950 17970 17990  
AGCCTGGGGCCCCAGTCCTTAGGGGACAACATATCCTCCTCATTCTCAGCAGATCAAGTC  
-----+-----+-----+-----+-----+-----+-----+  
18010 18030 18050  
CAGATGCCAAGATCCTGCCTCTGGTGAGAGGTAGCTCCTAAAATGAACAGATTTAAAGAC  
-----+-----+-----+-----+-----+-----+-----+  
18070 18090 18110  
AGGTGGCCACTGACAGCCACTCCAGGAACCTGAACTGCAGGGGCAGAGCCAGTGAATCAC  
-----+-----+-----+-----+-----+-----+-----+  
18130 18150 18170  
CGGACCTCCAGCACCTGCAGGCAGCTTGGAAGTTTCTTCCCCGAGTGGAGCTTCGACCCA  
-----+-----+-----+-----+-----+-----+-----+  
18190 18210 18230  
CCCACTCCAGGAACCCAGAGCCACATTAGAAGTTCCTGAGGGCTGGAGAACACTGCTGGG  
-----+-----+-----+-----+-----+-----+-----+

FIG. 29

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```
18250      18270      18290
CACACTCTCCAGCTCAATAAACCATCAGTCCCAGAAGCAAAGGTCACACAGCCCCTGACC
-----+-----+-----+-----+-----+-----+-----+

18310      18330      18350
TCCCTCACCAGTGGAGGCTGGGTAGTGCTGGCCATCCCAAAAGGGCTCTGTCCTGGGAGT
-----+-----+-----+-----+-----+-----+-----+

18370      18390      18410
CTGGTGTGTCTCCTACATGCAATTTCCACGGACCCAGCTCTGTGGAGGGCATGACTGCTG
-----+-----+-----+-----+-----+-----+-----+

18430      18450      18470
GCCAGAAGCTAGTGGTCCTGGGGCCCTATGGTTGCGACTGAGTCCACACTCCCCCTGCAGCC
-----+-----+-----+-----+-----+-----+-----+

18490      18510      18530
TGGCTGGCCTCTGCAAACAAACATAATTTGGGGACCTTCCTTCCTGTTTCTTCCCACCC
-----+-----+-----+-----+-----+-----+-----+

18550      18570      18590
TGTCTTCTCCCCTAGGTGGTTCCTGAGCCCCCACCCCAATCCCAGTGCTACACCTGAGG
-----+-----+-----+-----+-----+-----+-----+

18610      18630      18650
TTCTGGAGCTCAGAATCTGACAGCCTCTCCCCATTCTGTGTGTGTGCGGGGGACAGAGG
-----+-----+-----+-----+-----+-----+-----+

18670      18690      18710
GAACCATTTAAGAAAAGATACCAAAGTAGAAGTCAAAAGAAAGACATGTTGGCTATAGGC
-----+-----+-----+-----+-----+-----+-----+

18730      18750      18770
GTGGTGGCTCATGCCTATAATCCCAGCACTTTGGGAAGCCGGGGTAGGAGGATCACCAGA
-----+-----+-----+-----+-----+-----+-----+

18790      18810      18830
```

FIG. 29

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GGCCAGCAGGTCACACCAGCCTGGGCAACACAGCAAGACACCGCATCTACAGAAAAATT  
-----+-----+-----+-----+-----+-----+-----+  
18850 18870 18890  
TTAAAATTAGCTGGGCGTGGTGGTGTGTACCTGTAGGCCTAGCTGCTCAGGAGGCTGAAG  
-----+-----+-----+-----+-----+-----+-----+  
18910 18930 18950  
CAGGAGGATCACTTGAGCCTGAGTTCAACACTGCAGTGAGCTATGGTGGCACCCTGCAC  
-----+-----+-----+-----+-----+-----+-----+  
18970 18990 19010  
TCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCTAAAATAAATTTTAAAAGACATATTA  
-----+-----+-----+-----+-----+-----+-----+  
19030 19050 19070  
ACTTGACCTTGGTTAGTCTTTTCTGTATGTAAATTCAACCCATGGGGTGCCCTGAGGAC  
-----+-----+-----+-----+-----+-----+-----+  
19090 19110 19130  
CCACACGGGGTGGTGGTTGGCGGGGTGGTGGTTGGTGGGGTGGTGGCTGACGGGGTGGTG  
-----+-----+-----+-----+-----+-----+-----+  
19150 19170 19190  
GCTGGCAGGCCGAGCCTAGATGGCAGCCAGAGCCCCAGGCATGTGTCTGGGCACAGGACG  
-----+-----+-----+-----+-----+-----+-----+  
19210 19230 19250  
GTGTTGCCTAGTTTGAACACCCTCTTTGCTCTGTCACTCCTGCCCTCCCTTGGGCGTTTAC  
-----+-----+-----+-----+-----+-----+-----+  
19270 19290 19310  
ATTCTCCCATTGCTTCATGCAAGAGCTGCTGAGTGGCCTATATCAGCCAGCTGTTGCCGC  
-----+-----+-----+-----+-----+-----+-----+  
19330 19350 19370  
ATAACAAAACCATCCCAAACTGAGTGCAGGGAGGCAACTTCACCTCGGGCTCCACTCCA

FIG. 29

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```

-----+-----+-----+-----+-----+-----+
      19390              19410              19430
      .               .               .
CAAGCCCAAGGGGCCAGGTGAGAGTGCTCTCTAAAGCCCCCTCCTGCCTCAGTTGTAGTT
-----+-----+-----+-----+-----+-----+

      19450              19470              19490
      .               .               .
GCAAAATTTTAATTTATGAAGGTGACTGATGACACAGAGGCCAATGCTGTTGAAATAAGT
-----+-----+-----+-----+-----+-----+

      19510              19530              19550
      .               .               .
TATTACTCACAGTTTCCCACCATGCAGGGCCACAGTGGGGAGGCACTAGGTTTGGTCCAG
-----+-----+-----+-----+-----+-----+

      19570              19590              19610
      .               .               .
GGACAGAATCAGGAGCGAGTGGAAGGCACAGGCCACAGCCCACAGTGCCGTTTCCACTGG
-----+-----+-----+-----+-----+-----+

      19630              19650              19670
      .               .               .
GGAGGCAAGGCAGGCCAGGGGAAGAGGGTAGGATTGGCATTTTGAATCATTCTGGTGGGG
-----+-----+-----+-----+-----+-----+

      19690              19710              19730
      .               .               .
TTTGGGGCGTGGGGTTGGGCTCTAATTGTCTGGGTAGGTGCCTGGCCCTGAGCTGGTTTA
-----+-----+-----+-----+-----+-----+

      19750              19770              19790
      .               .               .
GGGCAGGGGAAATACTGGTTTCGTATGTGAGAGTTCCTTGAAGGGGGTGGTTGGTGTATG
-----+-----+-----+-----+-----+-----+

      19810              19830              19850
      .               .               .
GACTCAAGACTGGTCGGTTTGCATATGAAAGGCATGAGTTGTTTCTGATCTCCAGGAATC
-----+-----+-----+-----+-----+-----+

      19870              19890              19910
      .               .               .
AAGCAGTTTCTCTCCAGCCAACAAGCCCCACCCCGAGATGTTAAACCATCATAAATAG
-----+-----+-----+-----+-----+-----+

```

FIG. 29

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```
19930          19950          19970
.
AGAATCTAAGGCCAGGCATGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAG
-----+-----+-----+-----+-----+-----+-----+

19990          20010          20030
.
GCGGGAGGATCATTGAGGTGAGAGTTCGAGACCAGCCTGGCCAATGTGGTGAAACCCC
-----+-----+-----+-----+-----+-----+-----+

20050          20070          20090
.
ATCTCTACTAAAAATACAAAAATTAGCCCGGTGTGGTGGCACGTGCCTATAATCCCAGCT
-----+-----+-----+-----+-----+-----+-----+

20110          20130          20150
.
ACTCGGGAGGCTGCGGCAGGAGAATTGTTTGAACATGGGAGGTGGAGGTTGCAGTGAGCT
-----+-----+-----+-----+-----+-----+-----+

20170          20190          20210
.
GAGATCGTGCCACTGCACTCCAGCCTGGGCAACAAGAGCAAGACTCCGTCTCAAAAAAAA
-----+-----+-----+-----+-----+-----+-----+

20230          20250          20270
.
AAAAAAAAAAGAGAGACTCTAAAAATACACGTTAATATACCTCCCCCGCTCTTACCCT
-----+-----+-----+-----+-----+-----+-----+

20290          20310          20330
.
TCAGGAGGGGTGTCTAGACCCCGCGGACTCCAGCTACAAGGGACCCTGGGGAGGCCAA
-----+-----+-----+-----+-----+-----+-----+

20350          20370          20390
.
CTCTGCCCTCTTGGCTAATCCCAAGACTGCCAGCACCCCTCCACCCCTTCTCCATTC
-----+-----+-----+-----+-----+-----+-----+

20410          20430          20450
.
AGTGGCGAACCTGGGGAGGCCACGTGGGAAGGAAAGAGGGCTCTAAGAGGGGAGGCCCC
-----+-----+-----+-----+-----+-----+-----+

20470          20490          20510
.
AGACTGGGGGAGAGGCCTGTCTGGAGCCCAGGATCACCTGGCTGTGCTGCAGAACTGGAG
```

FIG. 29

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```
-----+-----+-----+-----+-----+-----+
      20530              20550              20570
AAGAGAAGCTCAGCAGAAAGGAGCTGGCATGGGGCCAACAGCAGAAAAGCAGGAGGCACG
-----+-----+-----+-----+-----+-----+

      20590              20610              20630
CAGAAGTGACTGGGAAGCAGGAGGGTAGGCATGGACCCTGAGGCTGAGCAGGAGGTACTG
-----+-----+-----+-----+-----+-----+

      20650              20670              20690
AGGGGCAGAGTGGACGCTGAGCTGGGGGTAGCGAGCGAGCCCAGCTCAGCTGTGACGCCC
-----+-----+-----+-----+-----+-----+

      20710              20730              20750
TCTGTTTGGCCACCCAACCTACCAGCTACTTGGGCTGCCCCGGGAGGAACTGGGCTTCCTC
-----+-----+-----+-----+-----+-----+

      20770              20790              20810
TGACATTCTGTGGCCTGCGGCCATCTGTGCACACCTTCTTCTCTCTGCCCCCTCCCTTGA
-----+-----+-----+-----+-----+-----+

      20830              20850              20870
CTTGTGGCACCCACAGACAGGTGGGAGAGTGTACCTGCCCTGTGTGGTCAGAGCTTGGTT
-----+-----+-----+-----+-----+-----+

      20890              20910              20930
TTGAGTTTCCTTCCCTCACCCCTCTTTCCTCCACACGCCAAAACACAAGAGGATGTGTC
-----+-----+-----+-----+-----+-----+

      20950              20970              20990
AGAGGCCTGTGAACCAGAGCAACTCCATCCTGAATAGGGGCTGAGCAAAATAAGGCTGAG
-----+-----+-----+-----+-----+-----+

      21010              21030              21050
ACCTACTGGGCTGCGTTTCCAGACAGTTACAGCATTCTGCGTCACAGGATGAGATAGGAG
-----+-----+-----+-----+-----+-----+
```

FIG. 29

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```
21070      21090      21110
ATACAGGTCATAAAGACCTTGCTGATAAAATAGTTTGCAGTAGGCCAGGCGCGGTAGCTC
-----+-----+-----+-----+-----+-----+-----+

21130      21150      21170
ACGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGGCGGATCACCTGAGGTCAGAAGT
-----+-----+-----+-----+-----+-----+-----+

21190      21210      21230
TCGAGACCAGCCTGGCCAACAAGGTGAAACCTCATCTCTACTAAAAATACAAAACTAGC
-----+-----+-----+-----+-----+-----+-----+

21250      21270      21290
CAGGCATGGTGGTGTGTGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCG
-----+-----+-----+-----+-----+-----+-----+

21310      21330      21350
CTTGAACCCAGGAGGTGGAGGTTGCAGTGAGCTGAGATCATGTCACTGCCTCCAGCCTG
-----+-----+-----+-----+-----+-----+-----+

21370      21390      21410
GAGCGAGACTCCGTCTCAAAAACCAAACCAACCAAAAAAATCAGCTTGCAATATAGAAGC
-----+-----+-----+-----+-----+-----+-----+

21430      21450      21470
TGGCTAAACCCACCCAAACCAAGATGGTGATGAGAGTGACCTCTGGTCGGTCCCCACTG
-----+-----+-----+-----+-----+-----+-----+

21490      21510      21530
CTCACTCCCACCAGCACCATGACAGGTTACAGATGCCATGGCAGTATCAGGAAGTTACC
-----+-----+-----+-----+-----+-----+-----+

21550      21570      21590
ATATATGGTCTAAAAAGGGGAGACATGAACAATCCACCCCTGTTTAGCAGATCATCCAGA
-----+-----+-----+-----+-----+-----+-----+

21610      21630      21650
AACAACCATAAAAAATGGGCAACCAGCAGCCCTCAGGGCTGCGCTCTCTATGGAGTAGCCA
-----+-----+-----+-----+-----+-----+-----+
```

FIG. 29

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```
-----+-----+-----+-----+-----+-----+
      21670              21690              21710
      .               .               .
TTCTTTTATTCTTTTACTTTCTTAATAAAATGTGCTTTCACTTTATGGACTCGTCTCAAAT
      .               .               .
-----+-----+-----+-----+-----+-----+

      21730              21750              21770
      .               .               .
TCTTTCTTGACGAGATCCAAGAACCCTCTCCTGGGGTCTGAATCTGGACCCCTTTCCGG
      .               .               .
-----+-----+-----+-----+-----+-----+

      21790              21810              21830
      .               .               .
TAACAGATGTCGTAGAGTGAAGCACAAACCACTGCAGGGGCATCTTGGTTTACATTTTGCT
      .               .               .
-----+-----+-----+-----+-----+-----+

      21850              21870              21890
      .               .               .
TCAGCGGCCATGGTTAGCACAGCGGAAAGCACATCACAGTCTTCTGATTCATTAAAAAAA
      .               .               .
-----+-----+-----+-----+-----+-----+

      21910              21930              21950
      .               .               .
TTAGGAAATGGACCACCACAAACCACAGACAGATGTACTGAGACAGGATAGGTAGTCAAG
      .               .               .
-----+-----+-----+-----+-----+-----+

      21970              21990              22010
      .               .               .
AAAGTGACCATGTTCTAGGCGCGCAGCAGCAACTGTGGTGACCGTACAGTCAACAAGCCT
      .               .               .
-----+-----+-----+-----+-----+-----+

      22030              22050              22070
      .               .               .
CAGCACTGGCATTGCAATTGAGCTCATTCAAGCAAAGCTATCTTCAGCAGGGACTTCTCC
      .               .               .
-----+-----+-----+-----+-----+-----+

      22090              22110              22130
      .               .               .
CTCTAGGCAGCAAGCGCATTTTTATTTTACCTGTCCTCAAAGTATCCTTTGCTCCTTAT
      .               .               .
-----+-----+-----+-----+-----+-----+

      22150              22170              22190
      .               .               .
AACAGTAAGGAACACACCCCTGTGTGGAGATTTAAGATGCTAATGAGGCCAAGCGCAGTT
      .               .               .
-----+-----+-----+-----+-----+-----+
```

FIG. 29



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22210	22230	22250
GCTCACGTCTGTAATTCCAGCACTTTGGGAGGCAGAGGTGGGCGGGTCACCTTGAGGTTAG		
-----+-----+-----+-----+-----+-----+-----+		
22270	22290	22310
AAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTCTACTAAAAATACAAAAAT		
-----+-----+-----+-----+-----+-----+-----+		
22330	22350	22370
TAGCCGGGCATGGTGGCGGGCGTCTGTAATCCCAGCTACCTGGGAGGCTGAGGCAGAAGA		
-----+-----+-----+-----+-----+-----+-----+		
22390	22410	22430
ATCGCTTGAACCTGGGAGGCGGAGGTTGCAGTGAGCCAAGATCGTGCCACTGCACTCCAG		
-----+-----+-----+-----+-----+-----+-----+		
22450	22470	22490
CCTGAGGGAGAGAGAGAGCAAGACATCGTTTTTGTGTTGTTGTTGTTGTTGTTGTTGTT		
-----+-----+-----+-----+-----+-----+-----+		
22510	22530	22550
TTTTAAAAAAGTCAAGACAAATCATAGTGGGGGCTTTTCTGGTCACTTTTAAATCTT		
-----+-----+-----+-----+-----+-----+-----+		
22570	22590	22610
AGTGTTGAGACTTTATTTGAGACAGGGCCTTACTCTGTTGCCAGGTTGGATGAGATTTT		
-----+-----+-----+-----+-----+-----+-----+		
22630	22650	22670
TAACCTCAATATTTACTTATAGAATAACTTTTTGGTTAGTCAAAACAATGCTGTGTCTCA		
-----+-----+-----+-----+-----+-----+-----+		
22690	22710	22730
TTCTGATCAGAATAAAACATCAGACAACCTCAAGAGAAACATTCTGCAAAATAACTGGCCA		
-----+-----+-----+-----+-----+-----+-----+		
22750	22770	22790
GGATTCTTCAAAAGTGTCAAGGGTAAAGATAAGGAAAGATGAAGGAACCTCCAGATTGAG		

FIG. 29

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```
-----+-----+-----+-----+-----+-----+
      22810              22830              22850
      .               .               .
GAGAATAAGGAGACAAC.TGTGATGTGGGATCCTAGAAATGGATCTTGGAAACAGAAAAAGGA
-----+-----+-----+-----+-----+-----+

      22870              22890              22910
      .               .               .
CATTAGTGGAAAAATGAGAAATGCAAAACAGTCTACAGTTTCGTTAACAGGATTGTACCA
-----+-----+-----+-----+-----+-----+

      22930              22950              22970
      .               .               .
AGGTTAGTTTCCTAGCTGTAATGATTGGACTATGATTAAGTAAGATGGACCATCAGGGGA
-----+-----+-----+-----+-----+-----+

      22990              23010              23030
      .               .               .
AGCTGGGTGAAGGGTGTAAGGAAAATGCTTACATTTTCCAACCTTTCTGCAAGTCTAAAA
-----+-----+-----+-----+-----+-----+

      23050              23070              23090
      .               .               .
TTAGTCAACAATAAGAAGTTTAAAAATAGGCCAGGCATGGTGGCTCACACCTGTCATCCTA
-----+-----+-----+-----+-----+-----+

      23110              23130              23150
      .               .               .
GCAC'TTTGAGAGGCCGAGGTGGGAGGATGGTTTGAGCCCAGGAGTTCAAGACCAGCCTGC
-----+-----+-----+-----+-----+-----+

      23170              23190              23210
      .               .               .
GCAATAGAGCGAGACCCCAACTCTATTCAAAAAAATTTTTTAAAGTTTAAATAGAATTA
-----+-----+-----+-----+-----+-----+

      23230              23250              23270
      .               .               .
TATAAAAAAGGAAAAGAAAAATGCTGTTTCATAGCGTTCCTAGTTTAGCATGGGAGAGAC
-----+-----+-----+-----+-----+-----+

      23290              23310              23330
      .               .               .
CAGGTCTCCCTGGGTGGTTGTCTGTGTGTGTGCTGGGTGTGCGTGGCAGGGCTAGTGTGT
-----+-----+-----+-----+-----+-----+
```

FIG. 29

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23350	23370	23390
GGGGTCCGTCTAGGCACATTCAGGCGCCGAATCCCGTGGCTCCCAGGTTTACCTGACGGT		
-----+-----+-----+-----+-----+-----+-----+		
23410	23430	23450
GCAGCCTGGGGTGGAGACTTAATGAGGGCGGGGAGTTGCTGCAGCAAAGGCTCCTCCCAG		
-----+-----+-----+-----+-----+-----+-----+		
23470	23490	23510
GGGTATCAGCGCAGACAGCTGGGTTTTCACTGTGCTCCTGCTCCAGAGGCACTAGGAAGG		
-----+-----+-----+-----+-----+-----+-----+		
23530	23550	23570
GGGCGCCTATCAGACTAGGACTCTGCCAGCCATCCTTCTCTGTTGAAGGTCCAGC		
-----+-----+-----+-----+-----+-----+-----+		

FIG. 29

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```

      10              30              50
CAGCTATGGGCTGGAGGCCCGGAGAGCTCGGGGGACCCCGTTGCTGCTGCTGCTACTAC
-----+-----+-----+-----+
MetGlyTrpArgProArgArgAlaArgGlyThrProLeuLeuLeuLeuLeuLeuL

      70              90              110
TGCTGCTGCTCTGGCCAGTGCCAGGCGCCGGGGTGCTTCAAGGACATATCCCTGGGCAGC
-----+-----+-----+-----+
euLeuLeuLeuTrpProValProGlyAlaGlyValLeuGlnGlyHisIleProGlyGlnP

      130             150             170
CAGTCACCCCGCACTGGGTCTGGATGGACAACCCTGGCGCACCGTCAGCCTGGAGGAGC
-----+-----+-----+-----+
roValThrProHisTrpValLeuAspGlyGlnProTrpArgThrValSerLeuGluGluP

      190             210             230
CGGTCTCGAAGCCAGACATGGGGCTGGTGGCCCTGGAGGCTGAAGGCCAGGAGCTCCTGC
-----+-----+-----+-----+
roValSerLysProAspMetGlyLeuValAlaLeuGluAlaGluGlyGlnGluLeuLeuL

      250             270             290
TTGAGCTGGAGAAGAACCACAGGCTGCTGGCCCCAGGATACATAGAAACCCACTACGGCC
-----+-----+-----+-----+
euGluLeuGluLysAsnHisArgLeuLeuAlaProGlyTyrIleGluThrHisTyrGlyP

      310             330             350
CAGATGGGCAGCCAGTGGTCTGGCCCCCAACCACACGGATCATTGCCACTACCAAGGGC
-----+-----+-----+-----+
roAspGlyGlnProValValLeuAlaProAsnHisThrAspHisCysHisTyrGlnGlyA

      370             390             410
GAGTAAGGGGCTTCCCCGACTCCTGGGTAGTCCTCTGCACCTGCTCTGGGATGAGTGGCC
-----+-----+-----+-----+
rgValArgGlyPheProAspSerTrpValValLeuCysThrCysSerGlyMetSerGlyL

      430             450             470
TGATCACCCCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCA
-----+-----+-----+-----+
euIleThrLeuSerArgAsnAlaSerTyrTyrLeuArgProTrpProProArgGlySerL

```

FIG. 30

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```

      490              510              530
AGGACTTCTCAACCCACGAGATCTTTCGGATGGAGCAGCTGCTCACCTGGAAAGGAACCT
-----+-----+-----+-----+-----+-----+-----+
ysAspPheSerThrHisGluIlePheArgMetGluGlnLeuLeuThrTrpLysGlyThrC

      550              570              590
GTGGCCACAGGGATCCTGGGAACAAAGCGGGCATGACCAGCCTTCCTGGTGGTCCCCAGA
-----+-----+-----+-----+-----+-----+-----+
ysGlyHisArgAspProGlyAsnLysAlaGlyMetThrSerLeuProGlyGlyProGlns

      610              630              650
GCAGGGGCAGGCGAGAAGCGCGCAGGACCCGGAAGTACCTGGAAGTGTACATTGTGGCAG
-----+-----+-----+-----+-----+-----+-----+
erArgGlyArgArgGluAlaArgArgThrArgLysTyrLeuGluLeuTyrIleValAlaA

      670              690              710
ACCACACCCTGTTCTTGACTCGGCACCGAACTTGAACCACACCAAACAGCGTCTCCTGG
-----+-----+-----+-----+-----+-----+-----+
spHisThrLeuPheLeuThrArgHisArgAsnLeuAsnHisThrLysGlnArgLeuLeuG

      730              750              770
AAGTCGCCAÄCTACGTGGACCAGCTTCTCAGGACTCTGGACATTCAGGTGGCGCTGACCG
-----+-----+-----+-----+-----+-----+-----+
luValAlaAsnTyrValAspGlnLeuLeuArgThrLeuAspIleGlnValAlaLeuThrL

      790              810              830
GCCTGGAGGTGTGGACCGAGCGGGACCGCAGCCGCGTCACGCAGGACGCCAACGCCACGC
-----+-----+-----+-----+-----+-----+-----+
lyLeuGluValTrpThrGluArgAspArgSerArgValThrGlnAspAlaAsnAlaThrL

      850              870              890
TCTGGGCCTTCCTGCAGTGGCGCCGGGGGCTGTGGGCGCAGCGGCCCCACGACTCCGCGC
-----+-----+-----+-----+-----+-----+-----+
euTrpAlaPheLeuGlnTrpArgArgGlyLeuTrpAlaGlnArgProHisAspSerAlaG

      910              930              950
AGCTGCTCACGGGCGCGCCTTCCAGGGCGCCACAGTGGGCCTGGCGCCCGTCGAGGGCA
-----+-----+-----+-----+-----+-----+-----+
lnLeuLeuThrGlyArgAlaPheGlnGlyAlaThrValGlyLeuAlaProValGluGlyM

```

FIG. 30

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```

      970              990              1010
TGTGCCGCGCCGAGAGCTCGGGAGGCGTGAGCACGGACCACTCGGAGCTCCCCATCGGCG
-----+-----+-----+-----+-----+-----+
etCysArgAlaGluSerSerGlyGlyValSerThrAspHisSerGluLeuProIleGlyA

      1030              1050              1070
CCGCAGCCACCATGGCCCATGAGATCGGCCACAGCCTCGGCCTCAGCCACGACCCCGACG
-----+-----+-----+-----+-----+-----+
laAlaAlaThrMetAlaHisGluIleGlyHisSerLeuGlyLeuSerHisAspProAspG

      1090              1110              1130
GCTGCTGCGTGGAGGCTGCGGCCGAGTCCGGAGGCTGCGTCATGGCTGCGGCCACCGGGC
-----+-----+-----+-----+-----+-----+
lyCysCysValGluAlaAlaAlaGluSerGlyGlyCysValMetAlaAlaAlaThrGlyH

      1150              1170              1190
ACCCGTTTCCGCGCGTGTTTCAAGCGCTGCAGCCGCCGCCAGCTGCGCGCCTTCTTCCGCA
-----+-----+-----+-----+-----+-----+
isProPheProArgValPheSerAlaCysSerArgArgGlnLeuArgAlaPhePheArgL

      1210              1230              1250
AGGGGGGCGGCGCTTGCTCTCCAATGCCCGGACCCCGGACTCCCGGTGCCGCCGCGCGC
-----+-----+-----+-----+-----+-----+
ysGlyGlyGlyAlaCysLeuSerAsnAlaProAspProGlyLeuProValProProAlaL

      1270              1290              1310
TCTGCGGGAACGGCTTCGTGGAAGCGGGCGAGGAGTGTGACTGCGGCCCTGGCCAGGAGT
-----+-----+-----+-----+-----+-----+
euCysGlyAsnGlyPheValGluAlaGlyGluGluCysAspCysGlyProGlyGlnGluc

      1330              1350              1370
GCCGCGACCTCTGCTGCTTTGCTCACAACCTGCTCGCTGCGCCCGGGGGCCAGTGCGCCC
-----+-----+-----+-----+-----+-----+
ysArgAspLeuCysCysPheAlaHisAsnCysSerLeuArgProGlyAlaGlnCysAlaH

      1390              1410              1430
ACGGGGACTGCTGCGTGCGCTGCCTGCTGAAGCCGGCTGGAGCGCTGTGCCGCCAGGCCA
-----+-----+-----+-----+-----+-----+
isGlyAspCysCysValArgCysLeuLeuLysProAlaGlyAlaLeuCysArgGlnAlaM

      1450              1470              1490

```

FIG. 30

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TGGGTGACTGTGACCTCCCTGAGTTTTGCACGGGCACCTCCTCCCCTGTCCCCCAGACG  
-----+-----+-----+-----+-----+-----+  
etGlyAspCysAspLeuProGluPheCysThrGlyThrSerSerHisCysProProAspV

1510 1530 1550  
TTTACCTACTGGACGGCTCACCTGTGCCAGGGGCAGTGGCTACTGCTGGGATGGCGCAT  
-----+-----+-----+-----+-----+-----+  
alTyrLeuLeuAspGlySerProCysAlaArgGlySerGlyTyrCysTrpAspGlyAlaC

1570 1590 1610  
GTCCCACGCTGGAGCAGCAGTGTGCCAGCAGCTCTGGGGGCCTGGCTCCCACCCAGCTCCCG  
-----+-----+-----+-----+-----+-----+  
ysProThrLeuGluGlnGlnCysGlnGlnLeuTrpGlyProGlySerHisProAlaProG

1630 1650 1670  
AGGCCTGTTTCCAGGTGGTGAACCTCTGCGGGAGATGCTCATGGAACTGCGGCCAGGACA  
-----+-----+-----+-----+-----+-----+  
luAlaCysPheGlnValValAsnSerAlaGlyAspAlaHisGlyAsnCysGlyGlnAspS

1690 1710 1730  
GCGAGGGCCACTTCCTGCCCTGTGCAGGGAGGGATGCCCTGTGTGGGAAGCTGCAGTGCC  
-----+-----+-----+-----+-----+-----+  
erGluGlyHisPheLeuProCysAlaGlyArgAspAlaLeuCysGlyLysLeuGlnCysG

1750 1770 1790  
AGGGTGGAAAGCCCCAGCCTGCTCGCACCGCACATGGTGCCAGTGGACTCTACCGTTCACC  
-----+-----+-----+-----+-----+-----+  
lnGlyGlyLysProSerLeuLeuAlaProHisMetValProValAspSerThrValHisL

1810 1830 1850  
TAGATGGCCAGGAAGTGACTTGTCGGGGAGCCTTGGCACTCCCCAGTGCCAGCTGGACC  
-----+-----+-----+-----+-----+-----+  
euAspGlyGlnGluValThrCysArgGlyAlaLeuAlaLeuProSerAlaGlnLeuAspL

1870 1890 1910  
TGCTTGGCCTGGGCCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAATGGTGTGCCAGA  
-----+-----+-----+-----+-----+-----+  
euLeuGlyLeuGlyLeuValGluProGlyThrGlnCysGlyProArgMetValCysGlnS

1930 1950 1970

FIG. 30

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GCAGGCGCTGCAGGAAGAATGCCTTCCAGGAGCTTCAGCGCTGCCTGACTGCCTGCCACA  
-----+-----+-----+-----+-----+-----+  
erArgArgCysArgLysAsnAlaPheGlnGluLeuGlnArgCysLeuThrAlaCysHisS

1990

2010

2030

GCCACGGGGTTTGAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCCACCCT  
-----+-----+-----+-----+-----+-----+  
erHisGlyValCysAsnSerAsnHisAsnCysHisCysAlaProGlyTrpAlaProProP

2050

2070

2090

TCTGTGACAAGCCAGGCTTTGGTGGCAGCATGGACAGTGGCCCTGTGCAGGCTGAAAACC  
-----+-----+-----+-----+-----+-----+  
heCysAspLysProGlyPheGlyGlySerMetAspSerGlyProValGlnAlaGluAsnH

2110

2130

2150

ATGACACCTTCCTGCTGGCCATGCTCCTCAGCGTCCTGCTGCCTCTGCTCCAGGGGCCG  
-----+-----+-----+-----+-----+-----+  
isAspThrPheLeuLeuAlaMetLeuLeuSerValLeuLeuProLeuLeuProGlyAlaG

2170

2190

2210

GCCTGGCCTGGTGTGCTACCGACTCCCAGGAGCCCATCTGCAGCGATGCAGCTGGGGCT  
-----+-----+-----+-----+-----+-----+  
lyLeuAlaTrpCysCysTyrArgLeuProGlyAlaHisLeuGlnArgCysSerTrpGlyC

2230

2250

2270

GCAGAAGGGACCCTGCGTGCACTGGCCCCAAAGATGGCCCCACACAGGGACCACCCCTGG  
-----+-----+-----+-----+-----+-----+  
ysArgArgAspProAlaCysSerGlyProLysAspGlyProHisArgAspHisProLeuG

2290

2310

2330

GCGGCGTTCACCCCATGGAGTTGGGCCCCACAGCCACTGGACAGCCCTGGCCCCCTGGACC  
-----+-----+-----+-----+-----+-----+  
lyGlyValHisProMetGluLeuGlyProThrAlaThrGlyGlnProTrpProLeuAspP

2350

2370

2390

CTGAGAACTCTCATGAGCCCAGCAGCCACCCTGAGAAGCCTCTGCCAGCAGTCTCGCCTG  
-----+-----+-----+-----+-----+-----+  
roGluAsnSerHisGluProSerSerHisProGluLysProLeuProAlaValSerProA

2410

2430

2450

ACCCCCAAGATCAAGTCCAGATGCCAAGATCCTGCCTCTGGTGAGAGGTAGCTCCTAAAA

FIG. 30



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```
-----+-----+-----+-----+-----+-----+
spProGlnAspGlnValGlnMetProArgSerCysLeuTrpEnd

      2470              2490              2510
      .               .               .
TGAACAGATTAAAGACAGGTGGCCACTGACAGCCACTCCAGGAAGTTGAACTGCAGGGG
-----+-----+-----+-----+-----+-----+

      2530              2550              2570
      .               .               .
CAGAGCCAGTGAATCACCGGACCTCCAGCACCTGCAGGCAGCTTGGAAAGTTTCTTCCCCG
-----+-----+-----+-----+-----+-----+

      2590              2610              2630
      .               .               .
AGTGGAGCTTCGACCCACCCACTCCAGGAACCCAGAGCCACATTAGAAGTTCCTGAGGGC
-----+-----+-----+-----+-----+-----+

      2650              2670              2690
      .               .               .
TGGAGAACTGCTGGGCACACTCTCCAGCTCAATAAACCATCAGTCCCAGAAGCAAAGG
-----+-----+-----+-----+-----+-----+

      2710              2730              2750
      .               .               .
TCACACAGCCCCTGACCTCCCTCACCAGTGGAGGCTGGGTAGTGCTGGCCATCCCAAAAG
-----+-----+-----+-----+-----+-----+

      2770              2790              2810
      .               .               .
GGCTCTGTCTCTGGGAGTCTGGTGTGTCTCTACATGCAATTTCCACGGACCCAGCTCTGT
-----+-----+-----+-----+-----+-----+

      2830              2850              2870
      .               .               .
GGAGGGCATGACTGCTGGCCAGAAGCTAGTGGTCCTGGGGCCCTATGGTTCGACTGAGTC
-----+-----+-----+-----+-----+-----+

      2890              2910              2930
      .               .               .
CACACTCCCCTGCAGCCTGGCTGGCCTCTGCAAAACAAACATAATTTGGGGACCTTCCTT
-----+-----+-----+-----+-----+-----+

      2950              2970              2990
      .               .               .
CCTGTTTCTTCCCACCCTGTCTTCTCCCCTAGGTGGTTCCTGAGCCCCACCCCCAATCC
-----+-----+-----+-----+-----+-----+
```

FIG. 30

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```

3010          3030          3050
CAGTGTACACCTGAGGTTCTGGAGCTCAGAATCTGACAGCCTCTCCCCATTCTGTGTG
-----+-----+-----+-----+-----+-----+-----+

3070          3090          3110
TGTCGGGGGGACAGAGGGAACCATTTAAGAAAAGATACCAAAGTAGAAGTCAAAAGAAAG
-----+-----+-----+-----+-----+-----+-----+

3130          3150          3170
ACATGTTGGCTATAGGCGTGGTGGCTCATGCCTATAATCCAGCACTTTGGGAAGCCGGG
-----+-----+-----+-----+-----+-----+-----+

3190          3210          3230
GTAGGAGGATCACCAGAGGCCAGCAGGTCCACACCAGCCTGGGCAACACAGCAAGACACC
-----+-----+-----+-----+-----+-----+-----+

3250          3270          3290
GCATCTACAGAAAAATTTTAAATTAGCTGGGCGTGGTGGTGTGTACCTGTAGGCCTAGC
-----+-----+-----+-----+-----+-----+-----+

3310          3330          3350
TGCTCAGGAGGCTGAAGCAGGAGGATCACTTGAGCCTGAGTTCAACACTGCAGTGAGCTA
-----+-----+-----+-----+-----+-----+-----+

3370          3390          3410
TGGTGGCACCCTGCACTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCTAAAAATAAAT
-----+-----+-----+-----+-----+-----+-----+

3430          3450          3470
TTTAAAAAGACATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
-----+-----+-----+-----+-----+-----+-----+

3490
AAAAAAAAAAAAAAAAAAAAAAAAAAAA
-----+-----+-----+-----+-----+-----+-----+

```

FIG. 30

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10 30 50  
CGGGCACGGGTCGGCCGCAATCCAGCCTGGGCGGAGCCGGAGTTGCGAGCCGCTGCCTAG

70 90 110  
AGGCCGAGGAGCTCACAGCTATGGGCTGGAGCCCCGGAGAGCTCGGGGGACCCCGTTGC  
MetGlyTrpArgProArgArgAlaArgGlyThrProLeuL

130 150 170  
TGCTGCTGCTACTACTGCTGCTGCTCTGGCCAGTGCCAGGCGCCGGGGTGCTTCAAGGAC  
euLeuLeuLeuLeuLeuLeuLeuLeuTrpProValProGlyAlaGlyValLeuGlnGlyH

190 210 230  
ATATCCCTGGGCAGCCAGTCACCCCGCACTGGGTCCTGGATGGACAACCCTGGCGCACCG  
isIleProGlyGlnProValThrProHisTrpValLeuAspGlyGlnProTrpArgThrV

250 270 290  
TCAGCCTGGAGGAGCCGGTCTCGAAGCCAGACATGGGGCTGGTGGCCCTGGAGGCTGAAG  
alSerLeuGluGluProValSerLysProAspMetGlyLeuValAlaLeuGluAlaGluG

310 330  
GCCAGGAGCTCCTGCTTGAGCTGGAGAAGAACCACAGGC  
lyGlnGluLeuLeuLeuGluLeuGluLysAsnHisArg

FIG. 31

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```
      10              30              50
      .              .              .
CGGGCACGGGTCGGCCGCAATCCAGCCTGGGCGGAGCCGGAGTTGCGAGCCGCTGCCTAG
      .              .              .

      70              90              110
      .              .              .
AGGCCGAGGAGCTCACAGCTATGGGCTGGAGGCCCCGGAGAGCTCGGGGGACCCCGTTGC
      MetGlyTrpArgProArgArgAlaArgGlyThrProLeuL

      130              150              170
      .              .              .
TGCTGCTGCTACTACTGCTGCTGCTCTGGCCAGTGCCAGGCGCCGGGGTGCTTCAAGGAC
      euLeuLeuLeuLeuLeuLeuLeuTrpProValProGlyAlaGlyValLeuGlnGlyH

      190              210
      .              .
ATATCCCTGGGCAGCCAGTCACCCCGCACTGGGTCCTGGATGGAC
      isIleProGlyGlnProValThrProHisTrpValLeuAspGly
```

FIG. 32

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```

      10              30              50
GCCTAGAGGCCGAGGAGCTCACAGCTATGGGCTGGAGGCCCGGAGAGCTCGGGGGACCC
      MetGlyTrpArgProArgArgAlaArgGlyThrP

      70              90              110
CGTTGCTGCTGCTACTACTGCTGCTGCTGGCCAGTGCCAGGCGCCGGGGTGCTTC
      roLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuTrpProValProGlyAlaGlyValLeuG

      130             150             170
AAGGACATATCCCTGGGCAGCCAGTCACCCCGCACTGGGCTCTGGATGGACAACCCTGGC
      lnGlyHisIleProGlyGlnProValThrProHisTrpValLeuAspGlyGlnProTrpA

      190             210             230
GCACCGTCAGCCTGGAGGAGCCGGTCTCGAAGCCAGACATGGGGCTGGTGGCCCTGGAGG
      rgThrValSerLeuGluGluProValSerLysProAspMetGlyLeuValAlaLeuGluA

      250             270             290
CTGAAGGCCAGGAGCTCCTGCTTGAGCTGGAGAAGAACCACAGGCTGCTGGCCCCAGGAT
      laGluGlyGlnGluLeuLeuLeuGluLeuGluLysAsnHisArgLeuLeuAlaProGlyT

      310             330             350
ACATAGAAACCCACTACGGCCCAGATGGGCAGCCAGTGGTGCTGGCCCCCAACCACACGG
      yrIleGluThrHisTyrGlyProAspGlyGlnProValValLeuAlaProAsnHisThrV

      370             390             410
TGAGATGCTTCCATGGGCTCTGGGATGCACCGCCAGAGGATCATTGCCACTACCAAGGGC
      alArgCysPheHisGlyLeuTrpAspAlaProProGluAspHisCysHisTyrGlnGlyA

      430             450             470
GAGTAAGGGGCTTCCCCGACTCCTGGGTAGTCCTCTGCACCTGCTCTGGGATGAGTGGCC
      rgValArgGlyPheProAspSerTrpValValLeuCysThrCysSerGlyMetSerGlyL

      490             510             530
TGATCACCCCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCA
      euIleThrLeuSerArgAsnAlaSerTyrTyrLeuArgProTrpProProArgGlySerL

      550
AGGACTTCTCAACCCACGAGAT
      ysAspPheSerThrHisGlu

```

FIG. 33

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10 30 50  
GAGGCCGAGGAGCTCACAGCTATGGGCTGGAGGCCCGGAGAGCTCGGGGGACCCCGTTG  
MetGlyTrpArgProArgArgAlaArgGlyThrProLeu

70 90 110  
CTGCTGCTGCTACTACTGCTGCTGCTCTGGCCAGTGCCAGGCGCCGGGGTGCTTCAAGGA  
LeuLeuLeuLeuLeuLeuLeuLeuLeuTrpProValProGlyAlaGlyValLeuGlnGly

130 150 170  
CATATCCCTGGGCAGCCAGTCACCCCGCACTGGGTCTTGATGGACAACCCTGGCGCACC  
HisIleProGlyGlnProValThrProHisTrpValLeuAspGlyGlnProTrpArgThr

190 210 230  
GTCAGCCTGGAGGAGCCGGTCTCGAAGCCAGACATGGGGCTGGTGGCCCTGGAGGCTGAA  
ValSerLeuGluGluProValSerLysProAspMetGlyLeuValAlaLeuGluAlaGlu

250 270 290  
GGCCAGGAGCTCCTGCTTGAGCTGGAGAAGAACCATGGCCTGATCACCTCAGCAGGAAT  
GlyGlnGluLeuLeuLeuGluLeuGluLysAsnHisGlyLeuIleThrLeuSerArgAsn

310 330 350  
GCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGACTTCTCAACCCACGAG  
AlaSerTyrTyrLeuArgProTrpProProArgGlySerLysAspPheSerThrHisGlu

AT

FIG. 34

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10 30 50  
GAGGCCGAGGAGCTCACAGCTATGGGCTGGAGGCCCGGAGAGCTCGGGGGACCCCGTTG  
MetGlyTrpArgProArgArgAlaArgGlyThrProLeu

70 90 110  
CTGCTGCTGCTACTACTGCTGCTGCTCTGGCCAGTGCCAGGCGCCGGGGTGCTTCAAGGA  
LeuLeuLeuLeuLeuLeuLeuLeuLeuTrpProValProGlyAlaGlyValLeuGlnGly

130 150 170  
CATATCCCTGGGCAGCCAGTCACCCCGCACTGGGTCCTGGATGGACAACCCTGGCGCACC  
HisIleProGlyGlnProValThrProHisTrpValLeuAspGlyGlnProTrpArgThr

190 210 230  
GTCAGCCTGGAGGAGCCGGTCTCGAAGCCAGACATGGGGCTGGTGGCCCTGGAGGCTGAA  
ValSerLeuGluGluProValSerLysProAspMetGlyLeuValAlaLeuGluAlaGlu

250 270 290  
GGCCAGGAGCTCCTGCTTGAGCTGGAGAAGAACCACAGGCTGCTGGCCCCAGGATACATA  
GlyGlnGluLeuLeuLeuGluLeuGluLysAsnHisArgLeuLeuAlaProGlyTyrIle

310 330 350  
GAAACCCACTACGGCCCAGATGGGCAGCCAGTGGTGCTGGCCCCCAACCACACGGATCAT  
GluThrHisTyrGlyProAspGlyGlnProValValLeuAlaProAsnHisThrAspHis

370 390 410  
TGCCACTACCAAGGGCGAGTAAGGGGCTTCCCCGACTCCTGGGTAGTCCTCTGCACCTGC  
CysHisTyrGlnGlyArgValArgGlyPheProAspSerTrpValValLeuCysThrCys

430 450 470  
TCTGGGATGAGTGGCCTGATCACCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGG  
SerGlyMetSerGlyLeuIleThrLeuSerArgAsnAlaSerTyrTyrLeuArgProTrp

490 510  
CCACCCCGGGGCTCCAAGGACTTCTCAACCCACGAGAT  
ProProArgGlySerLysAspPheSerThrHisGlu

FIG. 35

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10	30	50
CTGGCCCCAGGATACATAGAAACCCACTACGGCCCAGATGGGCAGCCAGTGGTGCTGGCC		
LeuAlaProGlyTyrIleGluThrHisTyrGlyProAspGlyGlnProValValLeuAla		
70	90	110
CCCAACCACACGGATCATTGCCACTACCAAGGGCGAGTAAGGGGCTTCCCCGACTCCTGG		
ProAsnHisThrAspHisCysHisTyrGlnGlyArgValArgGlyPheProAspSerTrp		
130	150	170
GTAGTCCTCTGCACCTGCTCTGGGATGAGTGGCCTGATCACCTCAGCAGGAATGCCAGC		
ValValLeuCysThrCysSerGlyMetSerGlyLeuIleThrLeuSerArgAsnAlaSer		
190	210	230
TATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGACTTCTCAACCCACGAGATCTTT		
TyrTyrLeuArgProTrpProProArgGlySerLysAspPheSerThrHisGluIlePhe		
250	270	290
CGGATGGAGCAGCTGCTCACCTGGAAAGGAACCTGTGGCCACAGGGATCCTGGGAACAAA		
ArgMetGluGlnLeuLeuThrTrpLysGlyThrCysGlyHisArgAspProGlyAsnLys		
310	330	350
GCGGGCATGACCAGCCTTCTGGTGGTCCCCAGAGCAGGGGCAGGCGAAAAGCGCGCAGG		
AlaGlyMetThrSerLeuProGlyGlyProGlnSerArgGlyArgArgLysAlaArgArg		
Glu		
370	390	410
ACCCGGAAGTACCTGGAAGTGTACATTGTGGCAGACCACACCCTGTTCTTGAAGTCCGGCAC		
ThrArgLysTyrLeuGluLeuTyrIleValAlaAspHisThrLeuPheLeuThrArgHis		
430	450	470
CGAACTTGAACACACCAAACAGCGTCTCCTGGAAGTCGCCAACTACGTGGACCAGCTT		
ArgAsnLeuAsnHisThrLysGlnArgLeuLeuGluValAlaAsnTyrValAspGlnLeu		
490		
CTCAGGACTCTGGACATTCAGGTGGC		
LeuArgThrLeuAspIleGlnVal		

FIG. 36



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10 30 50  
 CAGTGGCTACTGCTGGGATGGCGCATGTCCCACGCTGGAGCAGCAGTGCCAGCAGCTCTG  
 SerGlyTyrCysTrpAspGlyAlaCysProThrLeuGluGlnGlnCysGlnGlnLeuTr

70 90 110  
 GGGGCCTGGCTCCCACCCAGCTCCCGAGGCCCTGTTCCAGGTGGTGAACCTCTGCGGGAGA  
 pGlyProGlySerHisProAlaProGluAlaCysPheGlnValValAsnSerAlaGlyAs

130 150 170  
 TGCTCATGGAACTGCGGCCAGGACAGCGAGGGCCACTTCCTGCCCTGTGCAGGGAGGGA  
 pAlaHisGlyAsnCysGlyGlnAspSerGluGlyHisPheLeuProCysAlaGlyArgAs

190 210 230  
 TGCCCTGTGTGGGAAGCTGCAGTGCCAGGGTGGAAAGCCCAGCCTGCTCGCACCGCACAT  
 pAlaLeuCysGlyLysLeuGlnCysGlnGlyGlyLysProSerLeuLeuAlaProHisMe

250 270 290  
 GGTGCCAGTGGACTCTACCGTTACCTAGATGGCCAGGAAGTGACTTGTCGGGGAGCCTT  
 tValProValAspSerThrValHisLeuAspGlyGlnGluValThrCysArgGlyAlaLe

310 330 350  
 GGCACTCCCCAGTGCCAGCTGGACCTGCTTGGCCTGGGCCTGGTAGAGCCAGGCACCCA  
 uAlaLeuProSerAlaGlnLeuAspLeuLeuGlyLeuGlyLeuValGluProGlyThrGl

370 390 410  
 GTGTGGACCTAGAATGGTTTGCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGC  
 nCysGlyProArgMetValCysAsnSerAsnHisAsnCysHisCysAlaProGlyTrpAl

430 450 470  
 TCCACCCTTCTGTGACAAGCCAGGCTTTGGTGGCAGCATGGACAGTGGCCCTGTGCAGGC  
 aProProPheCysAspLysProGlyPheGlyGlySerMetAspSerGlyProValGlnAl

490  
 TGAAAACCATGACACCTTCCTGC  
 aGluAsnHisAspThrPheLeu

FIG. 37

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```

      10              30              50
CAGTGGCTACTGCTGGGATGGCGCATGTCCCACGCTGGAGCAGCAGTGCCAGCAGCTCTG
SerGlyTyrCysTrpAspGlyAlaCysProThrLeuGluGlnGlnCysGlnGlnLeuTr

      70              90              110
GGGGCCTGGCTCCCACCCAGCTCCCAGGGCCTGTTTCCAGGTGGTGAACCTCGCGGGAGA
pGlyProGlySerHisProAlaProGluAlaCysPheGlnValValAsnSerAlaGlyAs

      130             150             170
TGCTCATGGAACTGCGGCCAGGACAGCGAGGGCCACTTCCTGCCCTGTGCAGGGAGGGA
pAlaHisGlyAsnCysGlyGlnAspSerGluGlyHisPheLeuProCysAlaGlyArgAs

      190             210             230
TGCCCTGTGTGGGAAGCTGCAGTGCCAGGGTGGAAAGCCCAGCCTGCTCGCACCGCACAT
pAlaLeuCysGlyLysLeuGlnCysGlnGlyGlyLysProSerLeuLeuAlaProHisMe

      250             270             290
GGTGCCAGTGGACTCTACCGTTCACCTAGATGGCCAGGAAGTGACTGTGCGGGAGCCTT
tValProValAspSerThrValHisLeuAspGlyGlnGluValThrCysArgGlyAlaLe

      310             330             350
GGCACTCCCCAGTGGCCAGCTGGACCTGCTTGGCCTGGGCCTGGTAGAGCCAGGCACCCA
uAlaLeuProSerAlaGlnLeuAspLeuLeuGlyLeuGlyLeuValGluProGlyThrGl

      370             390             410
GTGTGGACCTAGAATGGTGTGCCAGAGCAGGCGCTGCAGGAAGAATGCCTTCCAGGAGCT
nCysGlyProArgMetValCysGlnSerArgArgCysArgLysAsnAlaPheGlnGluLe

      430             450             470
TCAGCGCTGCCTGACTGCCTGCCACAGCCACGGGGTTGCAATAGCAACCATAACTGCCA
uGlnArgCysLeuThrAlaCysHisSerHisGlyValCysAsnSerAsnHisAsnCysHi

      490             510             530
CTGTGCTCCAGGCTGGGCTCCACCCTTCTGTGACAAGCCAGGCTTTGGTGGCAGCATGGA
sCysAlaProGlyTrpAlaProProPheCysAspLysProGlyPheGlyGlySerMetAs

      550             570
CAGTGGCCCTGTGCAGGCTGAAAACCATGACACCTTCCTGC
pSerGlyProValGlnAlaGluAsnHisAspThrPheLeu
```

FIG. 38

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```

      10              30              50
      .              .              .
CAGTGGCTACTGCTGGGATGGCGCATGTCCCACGCTGGAGCAGCAGTGCCAGCAGCTCTG
SerGlyTyrCysTrpAspGlyAlaCysProThrLeuGluGlnGlnCysGlnGlnLeuTr

      70              90              110
      .              .              .
GGGGCCTGATGGCCAGGAAGTGACTTGTCGGGGAGCCTTGGCACTCCCCAGTGCCCAGCT
pGlyProAspGlyGlnGluValThrCysArgGlyAlaLeuAlaLeuProSerAlaGlnLe

      130             150             170
      .              .              .
GGACCTGCTTGGCCTGGGCCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAATGGTGTG
uAspLeuLeuGlyLeuGlyLeuValGluProGlyThrGlnCysGlyProArgMetValCy

      190             210             230
      .              .              .
CCAGAGCAGGCGCTGCAGGAAGAATGCCTTCCAGGAGCTTCAGCGCTGCCTGACTGCCTG
sGlnSerArgArgCysArgLysAsnAlaPheGlnGluLeuGlnArgCysLeuThrAlaCy

      250             270             290
      .              .              .
CCACAGCCACGGGGTTTGCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCC
sHisSerHisGlyValCysAsnSerAsnHisAsnCysHisCysAlaProGlyTrpAlaPr

      310             330             350
      .              .              .
ACCCTTCTGTGACAAGCCAGGCTTTGGTGGCAGCATGGACAGTGGCCCTGTGCAGGCTGA
oProPheCysAspLysProGlyPheGlyGlySerMetAspSerGlyProValGlnAlaGl

      370
      .
AAACCATGACACCTTCCTGC
uAsnHisAspThrPheLeu

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FIG. 39

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10 30 50  
GGCCTGGTGTGCTACCGACTCCCAGGAGCCCATCTGCAGCGATGCAGCTGGGGCTGCAG  
AlaTrpCysCysTyrArgLeuProGlyAlaHisLeuGlnArgCysSerTrpGlyCysAr

70 90 110  
AAGGGACCCTGCGTGCACTGGCCCCAAAGATGGCCCACACAGGGACCACCCCTGGGCGG  
gArgAspProAlaCysSerGlyProLysAspGlyProHisArgAspHisProLeuGlyGl

130 150 170  
CGTTCACCCCATGGAGTTGGGCCCCACAGCCACTGGACAGCCCTGGCCCCCTGGACCCTGA  
yValHisProMetGluLeuGlyProThrAlaThrGlyGlnProTrpProLeuAspProGl

190 210 230  
GAACTCTCATGAGCCCAGCAGCCACCCTGAGAAGCCTCTGCCAGCAGTCTCGCCTGACCC  
uAsnSerHisGluProSerSerHisProGluLysProLeuProAlaValSerProAspPr

250 270 290  
CCAAGCAGATCAAGTCCAGATGCCAAGATCCTGCCTCTGGTGAGAGGTAGCTCCTAAAAT  
oGlnAlaAspGlnValGlnMetProArgSerCysLeuTrpEnd

310  
GAACAGATTTAAAGACAGGTGGCC

FIG. 40

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      10              30              50
CAGTGGCTACTGCTGGGATGGCGCATGTCCCAGCTGGAGCAGCAGTGCCAGCAGCTCTG
SerGlyTyrCysTrpAspGlyAlaCysProThrLeuGluGlnGlnCysGlnGlnLeuTr

      70              90              110
GGGGCCTGATGGCCAGGAAGTGACTTGTGGGGAGCCTTGGCACTCCCCAGTGCCAGCT
pGlyProAspGlyGlnGluValThrCysArgGlyAlaLeuAlaLeuProSerAlaGlnLe

      130             150             170
GGACCTGCTTGGCCTGGGCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAATGGTGTG
uAspLeuLeuGlyLeuGlyLeuValGluProGlyThrGlnCysGlyProArgMetValCy

      190             210             230
CCAGAGCAGGCGCTGCAGGAAGAATGCCTTCCAGGAGCTTCAGCGCTGCCTGACTGCCTG
sGlnSerArgArgCysArgLysAsnAlaPheGlnGluLeuGlnArgCysLeuThrAlaCy

      250             270             290
CCACAGCCACGGGGTTTGCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCC
sHisSerHisGlyValCysAsnSerAsnHisAsnCysHisCysAlaProGlyTrpAlaPr

      310             330             350
ACCCTTCTGTGACAAGCCAGGCTTTGGTGGCAGCATGGACAGTGGCCCTGTGCAGGCTGA
oProPheCysAspLysProGlyPheGlyGlySerMetAspSerGlyProValGlnAlaGl

      370             390             410
AAACCATGACACCTTCCTGCTGGCCATGCTCCTCAGCGTCTGCTGCCTTGCTCCCAGG
uAsnHisAspThrPheLeuLeuAlaMetLeuLeuSerValLeuLeuProLeuLeuProGl

      430             450             470
GGCCGGCCTGGCCTGGTGTGTGCTACCGACTCCCAGGAGCCCATCTGCAGCGATGCAGCTG
yAlaGlyLeuAlaTrpCysCysTyrArgLeuProGlyAlaHisLeuGlnArgCysSerTr

      490             510             530
GGGCTGCAGAAGGGACCCCTGCGTGCACTGGCCCCAAGATGGCCACACAGGGACCACCC
pGlyCysArgArgAspProAlaCysSerGlyProLysAspGlyProHisArgAspHisPr

      550             570             590
CCTGGGCGGCGTTACCCCATGGAGTTGGGCCCCACAGCCACTGGACAGCCCTGGCCCT
oLeuGlyGlyValHisProMetGluLeuGlyProThrAlaThrGlyGlnProTrpProLe

      610             630             650
GGACCCCTGAGAACTCTCATGAGCCCAGCAGCCACCCTGAGAAGCCTCTGCCAGCAGTCTC
uAspProGluAsnSerHisGluProSerSerHisProGluLysProLeuProAlaValSe

      670             690             710
GCCTGACCCCCAAGCAGATCAAGTCCAGATGCCAAGATCCTGCCTCTGGTGAGAGGTAGC
rProAspProGlnAlaAspGlnValGlnMetProArgSerCysLeuTrpEnd

      730             750
TCCTAAAATGAACAGATTTAAAGACAGGTGGCC

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FIG. 41

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      10              30              50
CAGTGGCTACTGCTGGGATGGCGCATGTCCCACGCTGGAGCAGCAGTGCCAGCAGCTCTG
SerGlyTyrCysTrpAspGlyAlaCysProThrLeuGluGlnGlnCysGlnGlnLeuTr

      70              90              110
GGGGCCTGGCTCCCACCCAGCTCCCGAGGCCTGTTTCCAGGTGGTGAACCTCTGCGGGAGA
pGlyProGlySerHisProAlaProGluAlaCysPheGlnValValAsnSerAlaGlyAs

      130             150             170
TGCTCATGGAACTGCGGCCAGGACAGCGAGGGCCACTTCCTGCCCTGTGCAGGGAGGGA
pAlaHisGlyAsnCysGlyGlnAspSerGluGlyHisPheLeuProCysAlaGlyArgAs

      190             210             230
TGCCCTGTGTGGGAAGCTGCAGTGCCAGGGTGGAAAGCCCAGCCTGCTCGCACCGCACAT
pAlaLeuCysGlyLysLeuGlnCysGlnGlyGlyLysProSerLeuLeuAlaProHisMe

      250             270             290
GGTGCCAGTGGACTCTACCGTTCACCTAGATGGCCAGGAAGTGACTTGTCGGGGAGCCTT
tValProValAspSerThrValHisLeuAspGlyGlnGluValThrCysArgGlyAlaLe

      310             330             350
GGCACTCCCCAGTGCCCGAGCTGGACCTGCTTGGCCTGGGCCTGGTAGAGCCAGGCACCCA
uAlaLeuProSerAlaGlnLeuAspLeuLeuGlyLeuGlyLeuValGluProGlyThrGl

      370             390             410
GTGTGGACCTAGAATGGTGTGCCAGAGCAGGCGCTGCAGGAAGAATGCCTTCCAGGAGCT
nCysGlyProArgMetValCysGlnSerArgArgCysArgLysAsnAlaPheGlnGluLe

      430             450             470
TCAGCGCTGCCTGACTGCCTGCCACAGCCACGGGGTTTGCAATAGCAACCATAACTGCCA
uGlnArgCysLeuThrAlaCysHisSerHisGlyValCysAsnSerAsnHisAsnCysHi

      490             510             530
CTGTGCTCCAGGCTGGGCTCCACCCTTCTGTGACAAGCCAGGCTTTGGTGGCAGCATGGA
sCysAlaProGlyTrpAlaProProPheCysAspLysProGlyPheGlyGlySerMetAs

      550             570             590
CAGTGGCCCTGTGCAGGCTGAAAACCATGACACCTTCCTGCTGGCCATGCTCCTCAGCGT
pSerGlyProValGlnAlaGluAsnHisAspThrPheLeuLeuAlaMetLeuLeuSerVa

      610             630             650
CCTGCTGCCTCTGCTCCCAGGGGCCGGCCTGGCCTGGTGTGCTACCGACTCCAGGAGC
lLeuLeuProLeuLeuProGlyAlaGlyLeuAlaTrpCysCysTyrArgLeuProGlyAl

      670             690             710

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FIG. 42

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CCATCTGCAGCGATGCAGCTGGGGCTGCAGAAGGGACCCTGCGTGCAGTGGCCCCAAAGA
aHisLeuGlnArgCysSerTrpGlyCysArgArgAspProAlaCysSerGlyProLysAs

      730              750              770
TGGCCACACAGGGACCACCCCTGGGCGGCGTTCACCCCATGGAGTTGGGCCCCACAGC
pGlyProHisArgAspHisProLeuGlyGlyValHisProMetGluLeuGlyProThrAl

      790              810              830
CACTGGACAGCCCTGGCCCTGGACCCTGAGAACTCTCATGAGCCCAGCAGCCACCCTGA
aThrGlyGlnProTrpProLeuAspProGluAsnSerHisGluProSerSerHisProGl

      850              870              890
GAAGCCTCTGCCAGCAGTCTCGCCTGACCCCCAAGATCAAGTCCAGATGCCAAGATCCTG
uLysProLeuProAlaValSerProAspProGlnAspGlnValGlnMetProArgSerCy

      910              930              950
CCTCTGGTGAGAGGTAGCTCCTAAAATGAACAGATTTAAAGACAGGTGGCCACTGACAGC
sLeuTrpEnd

      970              990              1010
CACTCCAGGAACCTTGAAGTGCAGGGGCAGAGCCAGTGAATCACCGGACCTCCAGCACCTG

     1030              1050              1070
CAGGCAGCTTGGAAGTTTCTTCCCCGAGTGGAGCTTCGACCCACCCACTCCAGGAACCCA

     1090              1110              1130
GAGCCACATTAGAAGTTCCTGAGGGCTGGAGAACACTGCTGGGCACACTCTCCAGCTCAA

     1150
TAAACCATCAGTCC

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FIG. 42

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10 30 50  
CAGTGGCTACTGCTGGGATGGCGCATGTCCCACGCTGGAGCAGCAGTGCCAGCAGCTCTG  
SerGlyTyrCysTrpAspGlyAlaCysProThrLeuGluGlnGlnCysGlnGlnLeuTr

70 90 110  
GGGGCCTGATGGCCAGGAAGTGACTTGTCTGGGGAGCCTTGGCACTCCCCAGTGCCAGCT  
pGlyProAspGlyGlnGluValThrCysArgGlyAlaLeuAlaLeuProSerAlaGlnLe

130 150 170  
GGACCTGCTTGGCCTGGGCCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAATGGTGTG  
uAspLeuLeuGlyLeuGlyLeuValGluProGlyThrGlnCysGlyProArgMetValCy

190 210 230  
CCAGAGCAGGCGCTGCAGGAAGAATGCCTTCCAGGAGCTTCAGCGCTGCCTGACTGCCTG  
sGlnSerArgArgCysArgLysAsnAlaPheGlnGluLeuGlnArgCysLeuThrAlaCy

250 270 290  
CCACAGCCACGGGGTTTGCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCC  
sHisSerHisGlyValCysAsnSerAsnHisAsnCysHisCysAlaProGlyTrpAlaPr

310 330 350  
ACCCTTCTGTGACAAGCCAGGCTTTGGTGGCAGCATGGACAGTGGCCCTGTGCAGGCTGA  
oProPheCysAspLysProGlyPheGlyGlySerMetAspSerGlyProValGlnAlaGl

370 390 410  
AAACCATGACACCTTCCTGCTGGCCATGCTCCTCAGCGTCCTGCTGCCTCTGCTCCCAGG  
uAsnHisAspThrPheLeuLeuAlaMetLeuLeuSerValLeuLeuProLeuLeuProGl

430 450 470  
GGCCGGCCTGGCCTGGTGTGCTACCGACTCCCAGGAGCCCATCTGCAGCGATGCAGCTG  
yAlaGlyLeuAlaTrpCysCysTyrArgLeuProGlyAlaHisLeuGlnArgCysSerTr

490 510 530  
GGGCTGCAGAAGGGACCCTGCGTGCAGTGGCCCCAAAGATGGCCACACAGGGACCACCC  
pGlyCysArgArgAspProAlaCysSerGlyProLysAspGlyProHisArgAspHisPr

550 570 590

FIG. 43



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CCTGGGCGGGCGTTCACCCCATGGAGTTGGGCCCCACAGCCACTGGACAGCCCTGGCCCCCT  
oLeuGlyGlyValHisProMetGluLeuGlyProThrAlaThrGlyGlnProTrpProLe

610

630

650

GGACCCTGAGAACTCTCATGAGCCCAGCAGCCACCCTGAGAAGCCTCTGCCAGCAGTCTC  
uAspProGluAsnSerHisGluProSerSerHisProGluLysProLeuProAlaValSe

670

690

710

GCCTGACCCCCAAGATCAAGTCCAGATGCCAAGATCCTGCCTCTGGTGAGAGGTAGCTCC  
rProAspProGlnAspGlnValGlnMetProArgSerCysLeuTrpEnd

730

750

770

TAAAATGAACAGATTTAAAGACAGGTGGCCACTGACAGCCACTCCAGGAACCTTGAACCTGC

790

810

830

AGGGGCAGAGCCAGTGAATCACCGGACCTCCAGCACCTGCAGGCAGCTTGGAAGTTTCTT

850

870

890

CCCCGAGTGGAGCTTCGACCCACCCACTCCAGGAACCCAGAGCCACATTAGAAGTTCCTG

910

930

950

AGGGCTGGAGAACACTGCTGGGCACACTCTCCAGCTCAATAAACCATCAGTCC

FIG. 43